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tetraodon n
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treponema d
zymomonas m
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cryptococcu
geobacillus
bordetella
magnaporthe
bacillus su
caenorhabdi
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euroglyphus
helicobacte
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oryza sativ
lycopersico
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oryza sativ
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G5K8E5_KRENLA
PTR.1_SCHPO.
Q4HL4Z_CAMLA
Q9YBW4_ARRPE
Q731G1_TREDE
Q5RNEGO_ZYMMO.
S5RNEGO_ZYMMO.
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Q8RWC1_ARATH
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Q9XLTG_ANASP
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Q196G3_CABEL
Q8C499_MOUSE
Q8C499_AGRTS
YTR1_AZGBR
QSUG1_4_HUMAN
QSUG1_4_HUMAN
QTUQ37_CHRVO
QSEQ0_9 CLUOT
QUOQ37_CHRVO
QSEQ0_9 CLUOT
Q99HA_4_BRAJA
Q4JXP6_CORJK
Q99HA_4_BRAJA
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Q57V1_9TRYP
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        GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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QATKAS 9 GIRZE
QSBDIT, BOVIN
QAWINZ, ASPFU
LRRNS, FUNAN
QAWENS, ASPEU
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QAWENS, ANOGA
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CYOJAT, ANOGA
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Gapop 10.0 , Gapext 0.5
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psoroptes o vibrio vuln rhodococcus candida alb candida alb

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Q59UM3_CANAL Q7PG16_ANOGA Q9VZ33_DROME

092G15_R 059UH0_CA

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005615; C:extracellular space; ISS.
GO; GO:0005615; C:extracellular space; ISS.
GO; GO:0005910; F:kinase inhibitor activity; ISS.
GO; GO:000592; P:acute-phase response; ISS.
GO; GO:000502; P:negative requiation of insulin receptor sig. . .; ISS.
GO; GO:0005007; P:pincoytosis; ISS.
GO; GO:005077; P:regulation of phagocytosis; ISS.
GO; GO:005077; P:regulation of inflammacory response; ISS.
GO; GO:005017; P:regulation of inflammacory response; ISS.
HITTEPPO; IPR001001; P:ret inh cystat.
InterPro; IPR001163; Prot inh cystat.
InterPro; IPR001163; Prot inh fetuin.
Pfam; PR0001; Cystatin; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 205:321-331(1992).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
-!- SIMILARITY: Belongs to the fetuin family.
-!- SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown W.M., Christie D.L., Saunders N.R., Nawratil P., Dziegielewska K.D., Mueller-Esterl W., "The nucleotide and deduced amino acid structures of sheep and pig fetuin. Common structural features of the mammalian fetuin family.";
                                                                                                                                                                                                                                                                   Ejkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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PROSITE; PS01255; FETUIN 2; 1.
Direct protein sequencing; Glycoprotein; Repeat; Signal.
                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-2-HS-2HS-2HS-2HS-2HS-2HS-2HS-3HS-2FETUA;
Sus scrofa (Pig).
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Cystatin-like 2.
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N-linked (GlCNAc. . .) (F
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NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE
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                                                   362 AA.
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PIR; S22395; S22395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92209519; PubMed=1372866;
                                              STANDARD;
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           FETUA PIG
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-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Liver and bone.
-i- PTM: Phosphorylated on serine residues.
-i- SIMILARITY: Belongs to the fetuin family.
-i- SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                                                                           TISSUE-Liver;
MEDLINE-90170937; PubMed=1689725;
MEDLINE-90170937; PubMed=1689725;
Dziegielewska K.D., Brown W.M., Casey S.J., Christie D.L.,
Foreman R.C., Hill R.M., Saunders N.R.;
The complete cDNA and amino acid sequence of bovine fetuin. Its
homology with alpha 218 glycoprotein and relation to other members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 19-123 AND 188-243.
MEDLINE=8719052; PubMed=2436943; DOI=10.1016/0014-5793(87)80010-8;
Christie D.L., Dziegielewska K.M., Hill R.M., Saunders N.R.;
"Fetuin: the bovine homologue of human alpha 2HS glycoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88087074, PubMed-2447075,
Yet M.G., Chin C.C.O., Wold F.;
The covalent seructure of individual N-linked glycopeptides from ovomucoid and asialofetuin.";
J. Biol. Chem. 263:111-117(1988).
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pisano A., Jardine D.R., Packer N.H., Farnsworth V., Carson W., Cartier P., Redmond J.W., Williams K.L., Gooley A.A.; "Identifying sites of glycosylation in proteins."; (In Townsend R.R., Hotchkiss A.T. Jr. (eds.); Techniques in glycobiology, pp.299-320, Marcel Dekker, New York (1996).
                                 01-0CT-1989 (Rel. 12, Created)
01-AVG-1990 (Rel. 15, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Asialofetuin)
Name-AHSG; Synonyms-FETUA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-81207262; PubMed=6165360;
Alcaraz G., Marti J., Moinler D., Fougereau M.;
"NHS-terminal asequence of calf fetuin.";
Biochem. Biophys. Res. Commun. 99:30-36(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 72-103 AND 144-187.
                                                                                                                                                                                                                                                                                                                                                                                                 the cystatin superfamily.";
J. Biol. Chem. 265:4354-4357(1990)
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  STANDARD;
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                   NCBI_TaxID=9913;
FETUA BOVIN
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Gaps

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Pred. No. 0.25;

Best Local Similarity 100. Matches 10; Conservative

us-10-772-537-4.rup

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco)
Ebkaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                       MEDLINE-5220519; Pubmed=1372866;
Brown W., Christie D.L., Saunders N.R., Nawratil P.,
Dziegielewska K.D., Mueller-Esterl W.;
The nucleotide and deduced amino acid structures of sheep and pig
fetuin. Common structural features of the mammalian fetuin family.";
Bur. J. Blochem. 205;321:331(1992).
-! SUBCELIULAR LOCATION: Secreted.
-! SIMILARITY: Belongs to the fetuin family.
-! SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 70% of the chains)
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5046E569789AA7DB CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Alpha-2-HS-glycoprotein-like protein (Fragment)
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Cystatin-like 2.
N-linked (GloNAc.)
N-linked (GloNAc.)
N-linked (GloNac.)
By similarity.
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Q9LLS7;
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318 HTFSGVASVE 327
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CARBOHYD
CARBOHYD
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                       R GO; GO:0005615; C:extracellular space; ISS.
R GO; GO:0005615; C:extracellular space; ISS.
R GO; GO:0005615; P:kinase inhibitor activity; ISS.
R GO; GO:0005635; P:acute-phase response; ISS.
R GO; GO:000652; P:negative regulation of bone mineralization; ISS.
R GO; GO:0046627; P:negative regulation of insulin receptor sig. . .; ISS.
R GO; GO:005076; P:positive regulation of insulin receptor sig. . .; ISS.
R GO; GO:005072; P:regulation of inflammatory response; ISS.
R GO; GO:005072; P:regulation of inflammatory response; ISS.
R InterPro; IPR000101; P:skeletal development; ISS.
R InterPro; IPR000101; P:ret inh cystat.
InterPro; IPR0010163; Prot inh fetuin.
R Ffam; PF00011; Cystatin; Z.
R RNSITE; PS01254; PETUIN 1; 1.
R RNSITE; PS01255; PETUIN 1; 1.
R ROSITE; PS01255; PETUIN 2; 1.
R ROSITE; PS01255; PETUIN 2; 1.
R PROSITE; PS01255; PETUIN 2; 1.
R PROSITE; PS01255; PETUIN 2; 1.
R PROSITE; PS01255; RETUIN 2; 1.
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01-APR-1993 (Rel. 25, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-2-HS-91ycoprotein precursor (Fetuin-A).
Name-AHSG; Synonyma-FETUA;
Ovis arises (Sheep).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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Cystatin-like 2.
Cleavage (by trypsin) (Potential).
N-linked (GlCNAc. ..).
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CH - VK (in Ref. 3).
T -> H (in Ref. 2).
IT -> H (in Ref. 2).
IT -> K (in Ref. 2).
IT -> P (in Ref. 2).
V -> P (in Ref. 2).
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N-linked [GlCNAc.)
/FTId=CAR 000062.
N-linked (GlCNAc.)
O-linked (GalNAc.)
O-linked (GalNAc.)
O-linked (GalNAc.)
O-linked (GalNAc.)
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NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 16-23.
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Pred. No. 1;
1; Mismatches
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Best Local Similarity 90.00,
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313 HTFSGVASVE 322
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359 AA;
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PIR, A35714, A3
G1ycoSulteDB;
G0, G0:0019211;
G0, G0:0016513;
G0, G0:0016513;
G0, G0:0016613;
G0; G0:0016617;
G0; G0:0016917;
G0; G0:0016917;
G0; G0:0016917;
G0; G0:0016917;
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C STRAIN=FVBLN; TISSUE=Liver, and Salivary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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MEDLINE=9223088; PubMed=1373325; DOI=10.1016/0167-4781(92)90522-2;
Yang F., Chen Z.-L., Bergeron J.M., Cupples R.L., Friedrichs W.E.;
"Human alpha 2-HS-glycoprotein/bovine fetuin homologue in mice:
identification and developmental regulation of the gene.";
Biochim. Biophys. Acta 1130:149-156(1992).
                                                                                    Wang J., Sheehan M., Brookman H., Timko M.P.; "Characterization of cDNAs differentially expressed in roots of tobacco (Nicotiana tabacum cv Burley 21) during the early stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129;
MEDLINE=98058938; PubMed=9395485; DOI=10.1074/jbc.272.50.31496;
Jahnen-Dechent W., Schinke T., Trindl A., Mueller-Esterl W.,
Sablitzky F., Kaiser S., Blessing M.;
"Cloning and targeted deletion of the mouse fetuin gene.";
J. Biol. Chem. 272:31496-31503(1997).
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P29695; 035634;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-2-HS-9lycoprotein precursor (Fetuin-A) (Countertrypin)
Name=Ahsg; Synonyms=Fetua;
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Pred. No. 6.3;
1; Mismatches 1; Indels
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Sheehan M.J., Wang J., Brookman H.E., Timko M.P.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156369; AAF865799.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                 53 AA; 5414 MW; F3D7491638DF4D34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             77.6%;
                                                                                                                                                      alkaloid biosynthesis.";
Plant Sci. 158:19-32(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HSFSGVASVE 10
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EMBL; 896534; AAB22070.1; -; mRNA.

EMBL; AF007900; AAB3118.1; -; Genomic_DNA.

EMBL; AJ002146; CAA05210.1; -; Genomic_DNA.

EMBL; BC012678; AAH19678.1; -; Genomic_DNA.

EMBL; BC013678; AAH19622.1; -; mRNA.

EMBL; BC019822; AAH19622.1; -; mRNA.

EMBL; EM
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerrfield Y.S.N., Mrzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences ";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                            Gaps
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Cystatin-like 1.
Cystatin-like 1.
Cystatin-like 2.
N-linked (GLONAc. ..) (Potential).
N-linked (GLONAc. ..) (Potential).
N-linked (GLONAc. ..) (Potential).
By similarity.
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1; Mismatches
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(Glycoprotein PP63) (59

352 AA.

PRT;

Kellerer M.,

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"The nucleotide and partial amino acid sequences of rat fetuin.
Identity with the natural tyrosine kinase inhibitor of the rat insulin
                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89354538; PubMed=2766355; DOI=10.1016/0092-8674(89)90098-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                          'Characterization of a natural inhibitor of the insulin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                 Auberger P., Falquerho L., Contreres J.O., Pages G., le Cam G., Rossi B., le Cam A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine kinase: cDNA cloning, purification, and anti-mitogenic
                                                                                                                                                                                                                                     MEDLINE=92174966; PubMed=1371750;
Rauth G., Poeschke O., Fink E., Eulitz M., Tippmer S., Kel
Haering H., Nawratil P., Haasemann M., Jahnen-Dechent W.,
                                              01-MR-1992 (Rel. 21, Created)
01-MR-1993 (Rel. 25, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-2-HS-glycoprotein precursor (Fecuin-A) (Gl
                                                                                                                                                                                                                                                                                                                                           3ur. J. Biochem. 204:523-529(1992).
                                                                                                                        Name=Ahsg; Synonyms=Fetua;
Rattus norvegicus (Rat).
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 58:631-640(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 98:209-216(1991).
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                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                   Mueller-Esterl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1860865
                      FETUA RAT P24090;
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                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-2-HS-GHYCOprotein precursor (Fetuin-A) (Countertrypin).
Name=AHSG; Synonyms-FETUA;
Meriones unguicularus (Mongolian jird) (Mongolian gerbil).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalla, Eutebria; Buarchontoglires; Glires; Rodentia; Sciurognathi,
Muroidea; Maridae; Gerbillinae, Meriones.
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INCENTO; IPRO00010; Prot inh cystat.
InterPro; IPR0001019; Prot inh cystat.
InterPro; IPR00013; Prot inh fetuin.
Pfem; PP00031; Cystatin; Z.
SWART; SWOMO43; CY; Z.
PROSITE; PS01254; FETUIN 1; 1.
PROSITE; PS01255; FETUIN 2; 1.
Direct protein sequencing; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62717A0F0DB2C6B1 CRC64;
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                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 19-38.
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Cystatin-like 2.
N-linked (GlCNAc...)
N-linked (GlCNAc...)
N-linked (GlCNAc...)
By similarity.
                                                                                                     348 AA.
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                                                                                                                                                                                                                                                                                                                   MEDLINE=97279057; PubMed=9133634;
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HSPSGVASVE 10
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les 8; Conserv
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Matches
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IDENTITY OF PP63 WITH FETUIN.
MEDLINE=92119718; Pubmed=1370655; DOI=10.1016/0092-8674(92)90200-V;
Brown W.M., Christie D.L., Dziegielewska K.M., Saunders N.R., Yang F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obnishi T., Arakaki N., Nakamura O., Hirono S., Daikuhara Y.;
"Purification, characterization, and studies on biosynthesis of a 59-
KDa bone stalic acid-containing protein (BSP) from rat mandible using
a monoclonal antibody. Evidence that 59-KDa BSP may be the rat
counterpart of human alpha 2-HS glycoprotein and is synthesized by
                           MEDLINE=91200667; PubMed=1849862; DOI=10.1016/0378-1119(91)90175-B; Falquerho L., Patey G., Paqureau L., Rossi V., Lahuna O., Szpirer J., Szpirar C., Levan G., le Cam A., Patnary structure of the rat gene encoding an inhibitor of the insulin receptor tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and sequence analysis of cDNA for a 59 kD bone statoporotein of the rat: demonstration that it is a counterpart of human alpha 2-HS glycoprotein and bovine fetuin.";
J. Bone Miner. Res. 8:367-377(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haasemann M., Nawratil P., Mueller-Esterl W.; "Rat tyrosine kinase inhibitor shows sequence similarity to human alpha 2-HS glycoprotein and bovine fetuin."; Blochem. J. 274:899-902(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 19-35; 51-64; 165-180; 231-247 AND 327-348.
TISSUE=Mandible;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93206661; PubMed-7681247;·
Ohnishi T., Nakamura O., Ozawa M., Arakaki N., Muramateu T.,
Dalkuhara Y.;
NUCLEOTIDE SEQUENCE, AND SEQUENCE REVISION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 266:14636-14645(1991).
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Name=Ahsg;
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R GO; GO: 0005615; C: extracellular space; ISS.

R GO; GO: 0005910; F: kinase inhibitor activity; NAS.

R GO; GO: 0005021; P: exquee presents; ISS.

R GO; GO: 00030303; P: enegative regulation of bone mineralization; ISS.

R GO; GO: 00030308; P: negative regulation of cell growth; IDA.

R GO; GO: 0005077; P: princeytoris; ISS.

R GO; GO: 0005077; P: princeytoris; ISS.

R GO; GO: 0005077; P: regulation of insulin receptor sig. . .; IDA.

R GO; GO: 0005077; P: princeytoris; ISS.

R GO; GO: 0005077; P: regulation of inflammatory response; ISS.

R GO; GO: 0005077; P: regulation of inflammatory response; ISS.

R GO; GO: 0005071; P: regulation of inflammatory response; ISS.

R GO; GO: 0005071; P: regulation of inflammatory response; ISS.

R GO; GO: 0005071; P: regulation of inflammatory response; ISS.

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R GO; GO: 0005071; P: regulation of inflammatory response; ISS.

R GO; GO: 0005071; P: regulation of inflammatory response; ISS.

R FROMORDA; Cyclatin; Z.

R FROSITE; PSO1255; FETUIN.2; 1.
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct protein sequencing; Glycoprotein; Phosphorylation; Repeat; Signal.

SiGNAL 1 18
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Cystatin-like 2.

Cleavage (by trypsin) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.
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80.0%; Pred. No. 45;
iive 1; Mismatches 1; Indels
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BEL; K64346; CAA45042.1; -; mRNA.
EMBL; D10261; BAA01101.1; -; mRNA.
PIR; A32827; A32827.
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352 AA;
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RA MEDINE=201een;
RA MEDINE=201een;
RA MEDINE=20188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA MEDINE=201888257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Mang J., Heish F.,
RA Altechul S.F., Jordan H., Moore T., Wang J., Heish F.,
RA Altechul S.F., Jordan H., Moore T., Wang J., Heish F.,
RA Bownstein M.J., Ugdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
RA Nilalon D.K., Muzny D.M., Soderien B.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Evarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases:
EMBL, BCO1118; AAH1118.1; -; mRNA.
SEQUENCE 352 AA; 37982 MW; 43564F60F3C7C90A CRC64;
                                                                                                                                                                                                                                             Created)
Last sequence update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                            352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.6%; Score 38; DB
80.0%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                          10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80...
Best Aconservative
Aconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTTP75 RAT PRELIMINARY;
Q7TP75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                         QSBKD2_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              Alpha-2-HS-glycoprotein.
                               |:|| |||||
306 HAFSPVASVE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 HAFSPVASVE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HSFSGVASVE 10
10
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1 HSFSGVASVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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Gaps

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8; Conservative

Best Loc Matches

Gaps

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Score 38; DB 2; Length 951; Pred. No. 1.3e+02; 2; Mismatches 1; Indels

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77.6%;
          Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                           874
                                                                                                                       1 HSFSGVASVE 10
                                                                                                                                                           |||:|| |:|
865 HSFAGVLSLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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SEQUENCE 165 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Blr0444 protein.
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=375;
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Q58DI7_BOV
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                                                                 A Xu C.S., Li W.Q., Li Y.C., Chang C.F., Zhao L.F., Ma H., Wang L., A Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY325170; AAP92571.1; -; mRNA.

GO; 6004686; F.C.YSteine protease inhibitor activity; IEA.

INTERPO; IPR00010; Prot_inh_cystat.

INTERPO; IPR001363; Prot_inh_fetuin.

R Pfan; PR00011; Cystatin; 2.

R PRART; SM00043; CY; 2.

R PROSITE; PS01255; FETUIN 1; 1.

R PROSITE; PS01255; FETUIN 1; 1.

R PROSITE; PS01255; FETUIN 1; 1.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
GRNames=FG1449.1;
Gibberella zeae PH-1.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FRB-2004) to the EMBL/GenBank/DDBJ databases -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2; Length 553;
Pred. No. 72;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 951 AA; 105375 MW; BFA31EBB8D189DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AACM01000435; EAA68223.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951 AA.
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80.0%;
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Q4HX59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 HAFSPVASVE 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HSFSGVASVE 10
                                                NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pooled;
BELINE-21180013; PubMed=11282978; DOI=10.1101/gr.170101;
Smith T.-P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
Casas B., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.;
Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                  Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 AA; 17283 MW; 72DA12AE99C2FC8B CRC64;
                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Leucine rich repeat neuronal 5.
Name=LRRN5;
                             165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradyrhizobium japonicum USDAIII.";
DNA Res. 9:189-197(2002).
EMBL; BA000040; BAC45709.1; -; Genomi
LErPPro; IPRO05132; Lipoprotein_13.
Pfam; PF03330; DPBB 1; 1.
TIGRPAMS; TIGRO0413; rlpa; 1.
                             PRT;
                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                              STRAIN=USDA 110;
MEDLINE=22484998; Pubmed=12597275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.5%;
70 BRAJA
QB9X70 BRAJA PRELIMINARY;
QB9X70;
01-UNV-2003 (TYEMBLYEL). 24,
01-JUN-2003 (TYEMBLYEL). 24,
                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                               OrderedLocusNames=blr0444;
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QSBDI7;
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Matches 7; Conservative
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Gaps

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Indels

Mismatches

Conservative

77.8%; Pred. No.

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Best Local Similarity
Matches 7; Conserv
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Arroya J., Berriman M., Abbe K., Archer D.B., Berneido C., Bennett J.,
Arroya J., Berriman M., Abbe K., Archer D.B., Berneido C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulsen R., Dyer P.S.,
Raman M., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Reller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
Kumagai T., Lafton A., Latge J.-P. Li, W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Mollina M., Monod M.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Mollina M., Monod M.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
Benning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
Machida M., Hall N., Barrell B., Denning D.W.,
Machida M., Hall N., Barrell B., Denning Lilamentous fungus
                                                                               Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L.,
Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.,
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                   75.5%; Score 37; DB 2; Length 370; 60.0%; Pred. No. 76;
libraries and construction of a gene index for cattle."; Genome Res. 11:626-630(2001).
                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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1, AAHF01000002; EAL92221.1; -; Genomic DNA.

10, PAHF0100002; EAL9221.1; -; Genomic DNA.

10, AAHF0100002; EAL92221.1; -; Genomic CNA.
                                                                                                                                                                                                                                                                                     SDBF4872C1CCFAB0 CRC64;
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Last annotation update)
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                                                                                                                                                                EMBL; BT021610; AAX46457.1; -; mRNA
InterPro; IPR001611; LRR.
InterPro; IPR03591; LRR Typ.
                                                                                                                                                                                                           Pfam; PF00560; LRR 1; 6.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00369; LRR TYP; 7.
Leucine-rich repeat; Repeat.
SEQUENCE 370 AA; 40791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q4WYN2;
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus Af293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q4WYN2_ASPFU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     135 HSFAGLASLQ 144
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                                                  NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                               TISSUE=Pooled
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                                                                                                                                   clones.";
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75.5%; Score 37; DB 2; Length 389;

Query Match

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
116011.1 protein (MZB10.6 protein).
Name=T16011.1; Synonyms=MZB10.6;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley., Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J., Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S., Faraman M., Fedorova N., Feldblyum T.V., Fischer R., Fosker N., Praser A., Garcia J.L., Garcia M.J., Goble A., Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=330879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Pujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC010871, AAF07825.1; -; Genomic_DNA.
EMBL, AC009326; AAD56319.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; Cimembrane; IEA.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
GO; GO:0005215; F:protein binding: IEA.
GO; GO:0005219; F:voltage-gated potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR000310; BTB POZ.
InterPro; IPR003131; K.tetra.
Ffam; PF02214; K.tetra; 1.
SMART; SM00225; BTB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.5%; Score 37; DB 2; Length 460; 88.9%; Pred. No. 96; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49278 MW; 59CCB10EE974649E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
ORFNames=Afu5g03060;
Aspergillus fumigatus Af293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4WEH8 ASPFU PRELIMINARY,
                                                                                                                                                  7_arath
Q9S7R7_arath preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460
                                            171 HDFSGVATV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SFSGVASVE 10
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STRAIN=Af293;
1 HSFSGVASV
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Q4WEH8 ASPFU
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Haas H., Harris D., Horluchi H., Huang J., Humphrey S., Jimenez J., Reller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Kulkarni R., Luge J.-P., Li W., Lord A., Lu C., Mangai T., Latge J.-P., Li W., Lord A., Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M., Mouyna I., Mulligan S., Murphy L., O'Noil S., Paulsen I., A. Pertea M., Price C., Pritchard B.L., Quall M.A., Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U., A. Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M., Renning C.M., Rutter S., Salzberg S.L., Sanchez M., Rodriguez-Pena J.M., Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S., A. Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus S. L. CAUTION: The sequence shown here is derived from an EMBL/Genbank/DbbJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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A Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chimaldi C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J.S., Grimaldi C., Gu C., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liso D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.; The secreted protein discovery initiative (SpDI), a large-scale fort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRRNS HUMAN STANDARD; PRT; 713 AA.
075325; GSTOVO; QGUXMO; QBN182;
116-0CT-2001 (Rel. 40, Created)
110-MAY-2005 (Rel. 47, Last sequence update)
110-MAY-2005 (Rel. 48, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 48, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 48, Last annotation update)
110-MAY-2005 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.5%; Score 37; DB 2; Length 487; 60.0%; Pred. No. 1e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AAHF01000011; EAL85999.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 487 AA; 53160 MM; 8FFES0F97AB80CD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene 16:2997-3002(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Glial tumor;
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LRRN5 HUMAN
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PROSITE; PS50835; IG LIKE; 1.
Clycoprotein; Immunoglobulin domain; Leucine-rich repeat;
Clycoprotein; Immunoglobulin domain; Leucine-rich repeat;
Polymorphism; Repeat; Signal; Transmembrane.
SIGNAL 1 Potential.
713 Leucine-rich repeats neuronal protein 5.
                                                                                                                                                                                                                                                                                                                                       and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- SUBCELLULAR LOCATION: Type I membrane procein (Potential).

-!- TISSUE SPECIFICITY: Oversamplified in mallynant gliomas.

-!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
            NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Human chromosome 1 international sequencing consortium;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF030435; AAC39792.1; -; mENA.
EMBL; AX358290; AAQ88657.1; -; mENA.
EMBL; AL512306; CAI14096.1; -; Genomic_DNA.
EMBL; BC034047; AAH34047.1; -; mENA.
EMBL; BC068541; AAH68541.1; -; mENA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004872; F:receptor activity; TAS. GO; GO:0007155; P:cell adhesion; TAS. GO; GO:0007165; P:signal transduction; TAS.
                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P07359; 1P9A.
Ensembl; ENSG0000170382; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003885; LRR_Cygt.
InterPro; IPR003591; LRR_Cyp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00408; IGC2; 1.
SMART; SM00365; LRR SD22; 3.
SMART; SM00369; LRR_TYP; 10.
SMART; SM00082; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003598; Ig c2.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00019; LEURICHRPT.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC; HGNC:16914; LRRNS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00560; LRR 1; 9
Pfam; PF01463; LRRCT; 1
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Gaps

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MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE-22935763; PubMed=14574404; DOI=10.1038/nature02055;

MEDLINE-22935763; PubMed=14574404; DOI=10.1038/nature02055;

MINIMID L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,

Millming L., Jones M.C., Balleb G., Milne S., Ainscough R.,

Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.

Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.

Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.

Almeida J.P., Ambrose K.D., Marews T.D., Ashwell R.I.S.

Barlow K.F., Bates K., Bare D.M., Besaley H., Besaley O., Bird C.P.,

Barlow K.F., Bates K., Bare D.M., Besaley H., Besaley O., Bird C.P.,

Barlow K.F., Clark S., Clark G., Clee C.M., Cloeby V.,

Collier R.E., Collins J.E., Colman L.K., Corby N.R., Corby N.R.,

Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

Collier K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E.,

A collier K.M., Carner P., Garnet J., Graftm M.J.,

M. Gillson C.J., Glithero R.J., Graftm M.J.,

Gilby L.M., Gillson C.J., Glithero R.J., Graftm M.J.,

Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,

Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=20404861; PubMed=10949928; DOI=10.1038/sj.onc.1203716; Sasaki S., Ito E., Toki T., Maekawa T., Kanezaki R., Umenai T., Muto A., Nagai H., Kinoshita T., Yamamoto M., Inazawa J., Taketo M.M., Nakahata T., Igarashi K., Yokoyama M.; Nakahata T., Igarashi K., Yokoyama M.; BaCiloring and expression of human B cell-specific transcription factor BACH2 mapped to chromosome 6q15.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=21610689; PubMed=11746976; DOI=10.1002/gcc.1200;
Vieira S.A.D., Deininger M.W.N., Sorour A., Sinclair P., Foroni L.,
Goldman J.M., Melo J.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Transcription factor BACH2 is transcriptionally regulated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohara O., Nagase T., Kikuno F.R.;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       BACH2 HUMAN STANDARD;
Q9BYV9; Q59H70; Q5F793; Q9NTS;
28-FEB-2003 (Rel. 41, Created)
13-SFB-2003 (Rel. 48, Last annotation update)
Transcription regulator protein BACH2 (BTB and CNC homolog 2)
                                                                                                                                      75.5%; Score 37; DB 2; Length 750; 60.0%; Pred. No. 1.6e+02; ive 4; Mismatches 0; Indels
                                                                           1082; LRRCT; 1.
750 AA; 83237 MW; 2A5DDA7D8B58001A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCR/ABL oncogene.";
Genes Chromosomes Cancer 32:353-363(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
  PRINTS, PRO0019; LEURICHRPT.
SWART; SM00365; LRR SD22; 4.
SWART; SM00369; LRR_TYP; 8.
SWART; SM00082; LRRCT; 1.
SEQUENCE 750 AA; 83237 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                    Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                            304 HAFSGLASLQ 313
                                                                                                                                                                                                                                1 HSFSGVASVE 10
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=BACH2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
P -> L (in dbSNP:3789044).
/FIId=vAR_021921.
L -> V (in dbSNP:3747631).
/FIId=vAR_021922.
A -> T (in Ref. 2).
Y -> A (in Ref. 2).
Y -> C (in Ref. 4; AAH34047/AAH68541).
A -> P (in Ref. 4; AAH34047/AAH68541).
A -> P (in Ref. 4; AAH34047/AAH68541).
A -> P (in Ref. 4; AAH34047/AAH68541).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                  Potential.
Cytoplasmic (Potential).
LRR 1.
LRR 2.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
LRR 7.
LRR 9.
LRR 9.
LRR 11.
Ig-like C2-type.
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.5%; Score 37; DB 1; Length 713; 60.0%; Pred. No. 1.5e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
    Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP00000018422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AAABO1008807; EAA04464.2; -; Genomic_DNA.
InterPro; IPR001611; LRR.
InterPro; IPR001483; LRR_Cterm.
InterPro; IPR001885; LRR_Cyst.
InterPro; IPR0013891; LRR_Eyp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=ENSANGG0000015933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7QJA7_ANOGA PRELIMINARY;
Q7QJA7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 60.0
Matches 6; Conservative
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|135 HSFAGLASLQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HSFSGVASVE 10
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355 3
474 4
676 6
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TOPO DOM
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TOPO DOM
REPEAT
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DOMAIN
CARBOHYD
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215 AA.

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STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman R.S.L., Hufinagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphorylase).
Name=adk; OrderedLocusNames=PR3686;
                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
                                                                            KAD PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C., Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M., Loveland J., Martin S., Mabrieghi-Mohammadi M., Matchews L., Matchews L., McLaren S.J., McLay K., Matchews L., McLaren G.T., McLay K., McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T., Novik K.L., Oliver K., Overcon-Larty E.K., Parker A., Patel R., Perce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W., Porter K.M., Rameey Y., Rahby S.A., Rice C.M., Ross M.T., Sarale S.M., Schra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L., Steward C.A., Sycamore N., Tracey A., Troems A., Treter J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B., Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Whiteker H., Willey D.J., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                       Nature 425:885-811 (2003).

-I-FUNCTION: Transcriptional regulator that acts as repressor or activator. Binds to Mar recognition elements (MARE). Play important roles in coordinating transcription activation and repression by MAFK (By similarity).

-I-SUBBNIT: Heterodimer of BACH2 and Maf-related transcription factors (By similarity).

-I-SUBCELDUAR LOCATION: Nuclear (By similarity).

-I-SUBCELDUAR LOCATION: Nuclear (By similarity).

-I-SUBLECTICITY: B-cell specific.

-I-SIMILARITY: Contains 1 BTB (POZ) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSS0037; BTE; 1.
PROSITE; PSS0017; BZIP; 1.
PROSITE; PSS0017; BZIP; 1.
PROSITE; PS00036; BZIP=BASIC; 1.
Activator; DNA-binding; Nuclear protein; Repressor; Transcription; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF357835; AAK48898.1; -; mENA.
EMBL; AA271878; CAC28130.1; -; mENA.
EMBL; AB20889; BAD92126.1; ALT INIT; mENA.
EMBL; AL333692; CAL16237.1; -; Genomic DNA.
EMBL; AL121787; CAL16237.1; JOINED; Genomic_DNA.
EMBL; AL121787; CAL1648.1; -; Genomic_DNA.
EMBL; AL333692; CAL21648.1; JOINED; Genomic_DNA.
HSSP; POS412; LUNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V -> A (in Ref. 3).
L -> F (in Ref. 1).
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Basic motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANGFAC; T04795; -.
Ensembl; ENSG0000112182; Homo sapiens.
HGNC; HGNC:14078; BACH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poly-Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR000210; BTB POZ.
InterPro; IPR011616; bZIP 1.
InterPro; IPR004827; TF bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92537 MW;
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nes 6; Conservative
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666
169
75
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CONFLICT
SEQUENCE
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COMPBIAS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
Opportunistic pathogen.",
Nature 406:959-964(2000).
-I- FUNCTION: This small ubiquitous enzyme is essential for maintenance and cell growth.
-I- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
-I- SUBUNIT: Monomer (By similarity).
-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-I- SIMILARITY: Belongs to the adenylate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0113; ADENYLATE KINASE; 1.
ATP-binding; Complete proteome; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.5%; Score 36; DB 1; Length 215; 70.0%; Pred. No. 70; 1: Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 15 ATP (By similarity).
215 AA; 23107 MW; 744C9FDC51E1CO57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004788; AAG07074.1; -; Genomic_DNA.
PIR; G83184; G83184.
HSSP; PD55082; 1E4V.
HAMAP; MF 00235; -; 1.
InterPro; IPR01769; Ad Ct kin N.
InterPro; IPR006259; Adenylate kin.
InterPro; IPR00850; Adenylate kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094GN4 ORYSA PRELIMINARY; PRT; 094GN4 001-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00406; ADK; 1.
Pfam; PF05191; ADK lid; 1.
PRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate_Kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR01351; adk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
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195 HSIAGVGSVE 204
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Q94GN4_ORYSA
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||:||:|::: 446 HSYSGVSSLD 455

1 HSFSGVASVE 10

8 g .; IEA.

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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO000007937 (Fragment)
0RFNames=ENSANGG0000005991;
Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
GO; GO:0000155; F:two-component sensor molecule activity; IEA.

GO; GO:0000160; P:two-component signal transduction; IEA.

GO; GO:0000160; P:two-component signal transduction system (p. ..;

R InterPro; IPR00364; ATPBind ArPase.

R InterPro; IPR003661; His kinase.

R InterPro; IPR003661; His kinase.

R InterPro; IPR001610; PAC.

R InterPro; IPR001610; PAC.

R InterPro; IPR001610; PAC.

R InterPro; IPR001610; PAC.

R InterPro; IPR001696; V4R.

R InterPro; IPR001696; V4R.

R Pfam; PF00512; HisKA; I.

R Pfam; PF00512; HisKA; I.

R Pfam; PF00512; HisKA; I.

R Pfam; PR00369; PAG.

R Pfam; PR00369; PAG.

R Pfam; PR00349; PAG.

R PRINTS; PR00344; HATPASEC.

R SWART; SW00388; HATPASEC.

R SWART; SW00388; HATPASEC.

R SWART; SW00388; HATPASEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712 AA; 79069 MW; 094CD5076650F901 CRC64;
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GO; GO:0016491; F:ocfactor binding; IEA.
GO; GO:0016491; F:ocidector binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008170; F:transferase activity; IEA.
GO; GO:0008170; F:transferase activity; IEA.
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR001981; ACP_like.
InterPro; IPR001981; Adh_anferase.
InterPro; IPR001985; Acf_anferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%; Score 36; DB 2; Lei
60.0%; Pred. No. 2.4e+02;
ive 2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                        O7PYE4 ANOGA PRELIMINARY;
Q7PYE4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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STRAIN=PEST;
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Best Local Similarity
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                                                                                                                                                                                                Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K., Bhenner M., Bustrabeyn M., Tslirtin T., Riggs F., Haiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Hypothetical protein 031124_H03.28.
Hypothetical protein 031124_H03.28.
Name=031124 H03.28;
Oryza sativa (japonica cultivar-group).
Spermatophyta; Wagnoliophyta; Ereptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideee; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                               Gramene; Q94GN4; -...
Gramene; Q9005524; F:ATP binding; IEA.
GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
GO; GO:000413; F:Protein serine/threonine kinase activity; IEA.
GO; GO:000413; F:Protein amino acid phosphorylation; IEA.
InterPro: IRR008713; Ser thr.pkin.AS.
InterPro: IRR008713; Ser thr.pkin.AS.
InterPro: IRR008715; Tyr.pkin.ase.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Prot kinase, 2.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azoarcus sp. (strain EbN1).
Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
Rhodocyclaceae; Azoarcus.
NCBI_TaxID=76114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSP031;
01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hybrid sensor component of two-component regulation system.
OrderedLocusNames=AZOSEA30480; ORFNames=ebh5371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 36; DB 2; Length 407; 75.0%; Pred. No. 1.4e+02; ive. 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        White O., Fraser C.M.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC087852; AAK71566.1; -; Genomic_DNA.
HSSP; P08581; 1R1W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 protein.
407 AA; 44124 MW; DD4CB9AC2AF3EBCD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium, strain EbN1.";
Arch. Microbiol. 183:27-36(2005).
EMBL; CR553106; CA109173.1; -; Genomic_DNA.
GO:0016620; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016301; F:Kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.0%;
Matches 6; Conservative
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QSPOJI AZOSE PRELIMINARY;
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13 HSFSGISS 20
                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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STRAIN=EDN1;
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SEQUENCE 40
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ProDom; PD000158; Peptidase
SMART; SM00645; Pept_C1; 1
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QBI9P1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SFSGVASVE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         removed.
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA. GO:0016740; F:transferase activity; IEA. GO:0008270; F:zinc ion binding; IEA. GO:000633; P:fatty acid biosynthesis; IEA. GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47, Last enhydrase)
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                                                                                                                                                                                                                                                                                      Length 2232;
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                                                                                                                                                                                                                                                                                  73.5%; Score 36; DB.2; Length 223
60.0%; Pred. No. 7.9e+02;
Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                 NON TER 2232 2232
SEQUENCE 2232 AA, 246912 MW, FB38D692F96D1136 CRC64;
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Pfam; PF00109; ketcacyl-synt; 1.
Pfam; PF02801; Ketcacyl-synt; 1.
PROSITE; PS00606; B ETOACYL SYNTHASE; 1.
SEQUENCE 2342 AA; 262352 ÑW; A9052BBDAB9F05A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ueno K.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
InterPro; IPR006163; Phsppanteth_bind.
Pfam; PF00169; Acyl_transf 1; 1.
Pfam; PF00106; adh_short, 1.
Pfam; PF00107; ADH_zinc N; 1.
Pfam; PF00109; ketoacyl_synt; 1.
Pfam; PF02101; ketoacyl_synt C; 1.
PROSITE; PS50075; ACP_DOMAIN; 1.
PROSITE; PS00606; B KETOACYL_SYNTHASE; 1.
PROSITE; PS00095; C5_MTASE_2; UNRNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0004024; F: alcould wen, reflectivity, GO; GO: 0016740; F: transferase activity, GO; GO: 0008270; F: zinc ion binding; IEA. GO; GO: 0008633; P: fatty acid biosynthesis, GO; GO: 0008152; P: metabolism; IEA. InterPro; IPR001227; Ac transferase. R InterPro; IPR000794; KeToacyl_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67866; AAB53257.1; -; mRNA.
PIR; T18200; T18200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O01677_BOMMO PRELIMINARY;
                                                                                                                                                                                                                                                                                                    Local Similarity 60.0
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STRAIN-Kin-shu x Sho-wa;
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Best Local Similarity
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Q65VE3;
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001677_BOMMO
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Matches
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                               PubMed=15378067; DDI=10.1038/nbt1010; Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K., Kim G.H., Bong H., Hur C.G., Kim J.J.; "The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Derpl antigen (Fragment).

Bostroptes ovis (Sheep scab mite).

Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Sarcoptoidea;

Psoroptidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00406; -; 1.
InterPro; IPR010084; Fabz.
TIGRFAMS; TIGR01750; fabz; 1.
Complete proteome; Lipid A biosynthesis; Lipid synthesis; Lyase.
ACT_SITE 57 By similarity.
SEQUENCE 150 AA; 16861 MW; 5274EAA5EC20637B CRC64;
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A Mildr HR.P. Isaac R.E., Huntley J.F.,

A Mildr HR.P. Isaac R.E., Huntley J.F.,

I "Identification of an antigen from the sheep scab mite, Psoropt.

Tovis, homologous with house dust mite group I allergens.";

Parsaite Immunol. 24:413-422(2002).

-1- SIMILARITY: Belongs to the peptidase CI family.

R MSOP; P14080; 1YAL.

R MSOPS; CO1.073 -.

R GO; GO:000497; F:cysteine-type endopeptidase activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000169; Peptidase_CI.

R R InterPro; IPR000169; Peptidase_CI.

R ProDom; PP000112; Peptidase_CI; 1.

R ProDom; PP000112; Peptidase_CI; 1.

R SAMPN: SAMONGE. Peptidase_CI; 1.
Name-fabz; OrderedLocusNames-MS0460;
Mannheimia succiniciproducens (strain MBEL55E).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Biocechnol. 22:1275-1281(2004).
-!- FUNCTION: Involved in saturated fatty acids biosynthesis.
-!- SUBCELLUIAR LOCATION: Cycoplasmic (By similarity).
-!- SIMILARITY: Belongs to the thioester dehydratase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.4%; Score 35; DB 1; Length 150; 77.8%; Pred. No. 77; 1.1% 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 AA
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MEDLINE=22294898; PubMed=12406195;
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323 AA; 35542 MW; FIFD68B798032FD6 CRC64;
                            Query Match
Best Local Similarity
7, Conserve
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      SEQUENCE
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"The 20S proteasome of Streptcomyces coelicolor.";
J. Bacteriol. 180:5448-5453(1998).
EMBL; AF088800; Axc68687.1; -; Genomic_DNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                 Score 35, DB 2; Length 263;
Pred. No. 1.4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.4%; Score 35; DB 2; Length 308; 66.7%; Pred. No. 1.6e+02; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016809; AA007276.1; -; Genomic_DNA. HSSP; P11024; 1D40. GO; GO:0008746; F:NAD(P) transhydrogenase activity; IEA. GO; GO:0065118; P:electron transport; IEA. FirePro; IPRO04003; PNT_beta. Pfam; PF02233; PNTB; 1.
                                                                                        BF6DD21006DAB5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 308 AA; 32450 MW; 2541C7B818C5AF06 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Rhodococcus erythropolis.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NAD/NADP transhydrogenase beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 AA.
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PS00139; THIOL_PROTEASE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=98440439; PubMed=9765579;
                                                            263
29576 MW;
                                                                                                                                                 71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VIBVU
QBD751_VIBVU PRELIMINARY;
QBD751;
                                                                                                                  Ouery Match
Best Local Similarity 77.0.
The Conservative
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OSZGIS;
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51 HSFAGMAAV 59
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                                                                                     263 AA;
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hes 6; Conserva
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SEQUENCE
PROSITE;
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PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans,";
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=237561;
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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  Length 323;
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1, AACQ01000131; EAK94110.1; -; Genomic DNA.
ENCE 361 AA; 39579 MW; 50CD23F3DASFEC07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The diploid genome sequence of Candida albicans."; Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Potential zinc-binding dehydrogenase.
Name-F2D1; ORFNames-CaO19.9930;
Candida albicans SC5314.
                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
71.4%; Score 35; DB 2; Le 70.0%; Pred. No. 1.7e+02; tive 1; Mismatches 2;
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PubMed=15123810; DOI=10.1073/pnas.0401648101;
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                                                                                                                                                                                                                                                                                               PRT;
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10-MAY-2005 (TrEMBLrel. 30, Last seq
10-MAY-2005 (TrEMBLrel. 30, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=FZD1; ORFNames=CaO19.2394;
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Best Local Similarity 66، ۱۳
است 6، Conservative
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Q59UHO;
                                                     Conservative
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                                                                                                          1 HSFSGVASVE 10
                                                                                                                                                         HSLPGVSSVE 32
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557 AA.

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Q9VZ33_DROME PRELIMINARY;
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
Anophelinae, Anopheles.
NCBI_TAXID=180454;
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Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S.; "The diploid genome sequence of Candida albicans."; Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
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"Annotation of the Genome of Candida albicans.";
Submitted (APR-2004) to the BMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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,; AACQ01000130; EAK94161.1; -; Genomic DNA.
ENCE 361 AA; 39562 MW; A1F986832F7CGBA7 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR000379; Ser_estrs.
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ORFNames=ENSANGG00000020873;
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01-MAR-2004 (TrEMBLrel.
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297 HSYGGWTVE 306
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128 HSFEGAASI 136
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tes 6; Conserv
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107PGI ANO
107PGI ANO
107PGI O1-MA
DT 01-MA

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RESULT 31 Q9VZ33_DROME

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RUCLECTURE SEQUENCE.

REA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D.,

RA George R.A., Ledver S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Barton R.C., Rogers Y.H.C., Blazerj R.G., Champe M., Pfeiffer B.D.

RA Man K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Barottier B. C.,

RA Ballew R.M., Bauen D.A., Burler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davise P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davise P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davise P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davise P.,

RA Durbin K.J., Brangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,

RA Harris N.L., Harvey D.A., Heinan T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heinan T.J., Wei M.-H. Houck J.,

RA Harris N.L., Harvey D.A., Howland T.J., Wei M.-H., Ibegwan C.,

RA Adallel B.R., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Luk X., Jank M., Murph B., Murphy D.M., Nachlen B.,

Rakete B.R., Mollen K., Murphy B., Murphy D.M., Nachlen B.,

Rakete B.R., Noly M., Murphy B., Murphy B., Murphy B., Murphy B.,

Rakete B.W., Murphy B., Murphy B., Murphy B., Murphy B., Strong B.,

Rakete B.W., Murphy B., Warphier M., Strong R., Shell R.,

Rayer B.C., Spradling A.C., Spallecon M., Strong R., Shell R.,

Rayer B.C., Wasser B.W., Woodage T., Weiner E., Wang G., Zhan P., Hang G., Zhan P., Hang G., Zhan P., Hang G., Zhan P., Hang G., Zhang R., Mulliams S.M., Woodage T., Weiner E., Shen H., Weiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCLEOTIDE SEQUENCE.
MEDLINE-22446065; PubMed=12537568;
MEDLINE-22446065; PubMed=12537568;
MEDLINE-22446065; PubMed=12537568;
MEDLINE-22446065; PubMed=12537568;
MEDLINE-244606; Medler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Paches B.D., Kichards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Finishing a Whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hakapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                 Created)
                                                                                                          CG1961-PA.
Name=CG1961; ORFNames=CG1961;
                     Q9VZ33;
01-MAY-2000 (TrEMBLrel. 13,
                                                                                     01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a genomics perspective.";
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NUCLEOTIDE SEQUENCE.
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PRT;
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                                                                                                                                                                                                                                                                                                                                   71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Dyn. 225:384-391 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSXK85_XENLA PRELIMINARY;
                                                                                                                                                          Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 70.0
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  626 HSFRGVKEVE 635
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NUCLEOTIDE SEQUENCE.
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                      MUCLEOTIDE SEQUENCE.
MEDIINE=22426069; Pubmed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaninker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                            Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                                                                                                            'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Length 557; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                   "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases EMBL, AE003485; ARF47995.2; -; Genomic DNA. Ensembl; CG1961; Drosophila melanogaster. FlyBase; FBgn0030264; CG1961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1607; APYRAŠEFAMLY.
PROSITE; PS00785; 5 NUCLEOTIDASE 1; UNKNOWN 1.
SEQUENCE 557 AA; 61062 MW; 6160A3B3B9A9E068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 2 SCAF14738, whole genome shotgun sequence.
                                                                                                                                                            systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002).
                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 1004519; F: endonuclease activity; IEA. GO; GO: 1004519; F: hydrolase activity; IEA. GO; GO: 000166; F: hydrolase activity; IEA. GO; GO: 0000166; F: nucleotide binding; IEA. GO; GO: 0009166; P: nucleotide catabolism; IEA. InterPro; IPR006134; S'-Nucleotdase_C. InterPro; IPR00646; S'-Nucleotdase_N. InterPro; IPR006481; M-Pesterase. Pfam; PF02872; 5 nucleotid C: 1.
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70.0%;
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Q4S4P3;
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tes 7; Conserv
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Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Elemont C., Skalli Z., Catcolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesiron P., Bosak S., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Mincher P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the Leleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope; Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
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Pred. No. 6.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1176 AA; 131745 MW; 70CF69B8CB8193B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
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DOMAIN
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Q4HL42_CAM
                          RANGE OF STATES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA WOOD V., GAUlliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Rablone J. G., Beaham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Captule R., Connor R., Chullingworth T., Churcher C.M., Collins M., Connor R., Croin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgens K., James K.D., Jones M., Leather S., McDonald S., McLean J., Anens K., O'Neil S., Mensol M., Leather S., McDonald S., McLean J., Monorey P., Moule S., Mungall K.L., Murph, L.D., Niblett D., Odell C., Rah Mooney P., Moule S., Mungall K.L., Murph, L.D., Niblett D., Odell C., Rah Mooney P., Moule S., Mungall K.L., Murph, L.D., Niblett D., Odell C., Rah Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K., Stark S., Stevens K., Ander S., Moodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J.R., Nolckaert G., Aert R., Robben J., Grymonprez B., Moodward J.R., Nolcker M., Gallardin C., Holzer E., Moestl D., Andel C., Purbs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D., Andel C., Purbs M., Duesterhoeft A., Eritzc C., Holzer E., Moestl D., Andel C., Purbs M., Goffeau A., Gadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Losa M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benitco J., Shakovski G.V., Ussery D., Barrell B.G., Nurse P., Revelter B., Mallardin C., Parlace P., Are Spakovski G.V., Ussery D., Barrell B.G., Nurse P., Revelter B., Mallardin C., Parlace P., Revelter B., Mallardi
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
10-MNY-2005 (Rel. 47, Last annotation update)
E3 uniquitin protein ligase ptr1 (EC 6.3.2.-) (Poly(A)+ RNA transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%; Score 35; DB 2; Length 1414; 70.0%; Pred. No. 7.9e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
Klein S., Gerhard D.S.;
Submitted (Separd D.S.;
Submitted (Sep-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC083029; AAH83029.1; -; mRNA.
EMBL; BC083029; F:bydrolase activity; IEA.
InterPro; IPR000408; Reg.chr.condens.
PROSITE; PS0065; RC12; UNKNOWN 1.
SEQUENCE 1414 AA; 159671 MW; D9B35F9BF6DC2162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=ptrl; ORFNames=SPAC19D5.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HSFSGVASVE 10
                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896
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Matches
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PTR1_SCHPC
   RETAR BEREEF BEREFF BEREEF BEREFF BERFF BERF
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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        mRNA transport; Nuclear protein; Transport;
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L->Q: In ptr1-1; induces defects in mRNA
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Name=nusB; ORFNames=CLA0905;
Campylobacter lari RM2100.
Bacteria, Proteobacteria; Epsilonproteobacteria; Campylobacteraceae; Campylobacteraceae; Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN=RM2100;
Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the TOM1/FTR1 family.
SIMILARITY: Contains 1 HECT (EGAP-type E3 ubiquitin-protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 1; I
Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99531; CAB16714.1; -; Genomic_DNA.
PIR; T37964; T37964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTR, 13,500, 1C4Z,
HSSP, QOSO86, 1C4Z,
Genells Spombe; SPAC19D5.04; -.
GO; GO:0006406; P:mRNA-nucleus export; II
InterPro; IPR010309; DUF908 Ubiq iig.
InterPro; IPR010314; DUF913_Ubiq_lig.
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                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.4%;
75.0%;
AND MUTANT PTR1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF06012; DUF908; 1.
Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
PROSITE; PS50237; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4HL42_CAMLA PRELIMINARY;
Q4HL42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                    ligase) domain.
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ACT_SITE
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OSNRGO ZYMMO
ID OSNRGO ZYMMO PRELIMINARY;
                                                                                                                                                                                                                                                                                               6; Conservative
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Best Local Similarity
Matches 6; Conservat
                           NUCLEOTIDE SEOUENCE,
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                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zymomonas mobilis.
                                                                                                                                                                                                                  TIGR; TDE1903; -.
Complete proteome.
SEQUENCE 212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=542;
   NCBI_TaxID=158;
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Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U., Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                     Nelson K.E.; "Major structural and novel potential virulence mechanisms from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Membrane protein, putative.
Membrane protein, putative.
OrderedLocusNames=TDE1903;
Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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                                                              genomes of multiple Campylobacter species.", submitted (DEC-2004) to the BMI/GenBank/DBU databases.
-!- CAUTION: The sequence shown here is derived from an EMBI/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 2; Length 197;
Pred. No. 1.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                69.4%; Score 34; DB 2; Length 132; 60.0%; Pred. No. 1.1e+02; ive 1; Mismatches 3; Indels
                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae; Aeropyrum.
                                                                                                               preliminary data.
EMBL; AAFKO1000003; EALS4709.1; -; Genomic DNA.
SEQUENCE 132 AA; 15088 MW; A23FCDB486DC08D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Hypothetical protein.
SEQUENCE 197 AA; 21009 MW; 149882A258CC1B55 CRC64;
                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE1486.
OrderedLocusNames=APE1486;
                                                                                                                                                                                                                                                                                                           197 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99310339; PubMed=10382966;
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                                                                                                                                                   Query Match
Best Local Similarity 60.0%,
                                                                                                                                                                                                                                                                                                          Q9ybw4_Aerpe preliminary;
Q9ybw4;
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Q73LG1 TREDE PRELIMINARY;
Q73LG1;
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125 SFSGIASI 132
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                                                                                                                                                                                                                    1 HSFSGVASVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SFSGVASV 9
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    Aeropyrum pernix
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Pubmed=15592455; DOI=10.1038/hbt1045;
Seo J.-S. Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
"The genome sequence of the ethanologenic bacterium Zymomonas mobilis
PubMed=15664399; DOI=10.1073/pnas.0307639101; Heidelberg J.F., Sebhadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., Bodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H., Slengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F., Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A., Shateman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., Vabhishth P., McMed M.P., Smajs D., Howell J.K., Pal S., Amin A., Wahnisth P., McMed M.P., Smajs D., Howell J.K., Pal S., Amin A., Weinstock G.M., Norzis S.J., Fraser C.M., Paulsen I.T., "Comparison of the genome of the oral pathogen Treponema denticola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Zymomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 212
Pred, No. 1.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%; Score 34; DB 2; Length 223
66.7%; Pred. No. 1.9e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; Electron transport; Transport.
SEQUENCE 223 AA; 25648 MW; 942FDCFA595023CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AA; 24653 MW; 213875EDBFC7283F CRC64;
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Nat. Biotechnol. 23:63-68(2005).

EMBL. AE0069489; RAV88694.1; -; Genomic_DNA.

EMBL. AE0069489; R:electron transporter activity; IEA.

GO; GO:00045454; P:cell redox homeostasis; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR011767; GLR AS.

InterPro; IPR07494; Glutaredoxin2_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      with other spirochete genomes.";
Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
EMBL; AE017252; AAS12417.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA.
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InterPro; IPR012336; Thioredoxin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=grxB; OrderedLocusNames=ZMO0070;
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TIGRFAMs; TIGR02182; GRXB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00195, GLUTAREDOXIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%;
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the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
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                                                                                                           NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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027496 CAE
1D 027496
AC 027496
AC 02749
BD 01-NC
DT 01-NC
DT 01-NC
DT 01-NC
DE SERIA
OS CAENC
OC RABDE
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OC CAE
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STARBERE
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Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.,
"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AK222221 BAD95407.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicada S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sepurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Blemont C., Skalli Z., Cattolico D., Poulain J., De Berardinis V., Cruad C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-At3913750;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Wormlanes-GSTENGO0005699001;

Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Tetradontoidea; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF8089, whole genome shotgun sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 270 AA; 29597 MW; 6BCF4538A169957A CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                 270 AA
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                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAX-2005 (TrEMBLrel. 30, Galactosidase (Fragment).
                                                                                                                                                                                                                                                                                    Q56W18_ARATH PRELIMINARY;
Q56W18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TETNG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.4
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                  100 HSFSGIYSL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HSFSGVASVE 10
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                HSFSGVASV 9
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                                                                                                                                                                                                                                                                                                                                           Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Ensembl, PS583.4; Caenorhabditis elegans.

Wormbease, WBGene00009101, P25B3.4.

Wormbep, P25B3.4; CE05714.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR006483; M-pesterase.

InterPro; IPR0064843; M-pesterase.

Pfam; PF004189; Metallophos; 1.

PRINTS; PR00114; STPHHITASE.

SMART; SM00156; PP2AC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                             Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN 1.
Complete proteome; Hydrolase; Hypothetical procein; Iron.
SEQUENCE 291 AA; 33700 MW; 8561AA031886987B CRC64;
                                                                                                                                                                                                                                                                    / Match 69.4%; Score 34; DB 2; Length 286
Local Similarity 75.0%; Pred. No. 2.4e+02;
tes 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                               286 AA; 32391 MW; 79A2DCFC272A7F47 CRC64;
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--- SIMILARITY: Belongs to the PPP phosphatase family.
EMBL; Z70752; CAA94756.1; -; Genomic_DNA.
PIR; T21322; T21322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                027496 CAEEL PRELIMINARY; PRT; 291 AA. 027496; OI-NOV-1996 (TrEMBLrel. 01, Created) OI-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAV-2004 (TrEMBLrel. 26, Last annotation update) Serine/threonine protein phosphatase (EC 3.1.3.16). ORFNames=F2583.4;
                                                                                                                  preliminary data.
EMBL; CAAE01008089; CAF91137.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 HSPAGVAN 196
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Molecular analysis of the group 1 and 2 allergens from the house dust
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InterPro, IPR000668; Peptidase Cl.
PANTHER; PHH12411; Peptidase Cl. 1.
Pran, PR00112; Peptidase Cl. 1.
PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase Cl. 1.
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                                                                                       NUCLEOTIDE SEQUENCE OF 99-309
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025902 HELPY PRELIMINARY;
025902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 77.8 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 AFŚĠVASTE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SFSGVASVE 10
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19
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269
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289
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115
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116
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136
320
321 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
ACT_SITE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymogen.
SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    025902
ID 022
AC 022
DT 011
DT 011
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                                                                                                                                                                                                                                                                                                                                 Salanoubat M., Genin S., Artiguenave F., Golzy J., Mangenot S., Arla M., Bilault A., Brottier P., Camus J.C., Cattolico L., Chaider M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
Weissenbach J., Boucher C.A.;
Nature 415:497-502(2002).

-I- FUNCTION: Part of a binding-protein-dependent transport system. Probably responsible for the translocation of the substrate across the membrane (By similarity).

-I- SUBCELLUAR LOCATION: Integral membrane protein (By similarity).

-I- SUBCELLUAR LOCATION: Integral membrane protein transport transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; AL646665; CAD15233.1; -; Genomic_DNA.
G0:0019866; C:inner membrane; IEA.
G0:0015011; C:integral to membrane; IEA.
G0:0005115; F:inorganic phosphate transporter activity; IEA.
G0:0015114; F:phosphate transporter activity; IEA.
G0:0005115; F:ransporter activity; IEA.
G0:0006817; P:phosphate transport; IEA.
G0:0006817; P:phosphate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Acariformes, Sarcopliformes, Astigmata, Psoroptidia, Analgoidea,
Pyroglyphidae, Euroglyphus.
NCBI_TaxID=6958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P25706, 09T223; 09T224; 09UBA0; PKI; 321 AA.
P25706, 09T223; 09T224; 09UBA0; 01-MAY-1992 (Rel. 22, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mite group 1 allergen Eur m 1 precursor (EC 3.4.22.-) (Eur m I).
Name=EURM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.4%; Score 34; DB 2; Length 294; 66.7%; Pred. No. 2.5e+02; ive 1; Mismatches 2; Indels
                                                                              01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE PHOSPHATE TRANSMEMBRANE ABC TRANSPORTER PROTEIN.
Name-pstA, OrderedLocusNames-RSC1531, ORFNames-RS03773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE (EUR M 1.0101 AND EUR M 1.0102).
MEDLINE=99126275; PubMed=9925958; DOI=10.1159/000024026;
Smith W., Mills K., Hazell L., Hart B.J., Thomas W.;
                                                                                                                                                                                                                                                                                                                 MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 AA; 31443 MW; AFCB03B2AA581AB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euroglyphus maynei (Mayne's house dust mite).
                        294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Transmembrane; Transport
SEQUENCE 294 AA; 31443 MW; AFCB03B2AAS8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000515; BPD transp.
InterPro; IPR005672; Phosphate pstA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00528; BPD transp 1; 1.
TIGRFAMB; TIGR00974; 3a0107802c; 1.
PROSITE; PS50928; ABC_TM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system permease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%;
                     Q8XZ73_RALSO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |||:| |
150 HHFSGIAGV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HSFSGVASV 9
                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                     NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EURM1 BURMA
                                           08XZ73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EURMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
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                                                                                                                                                                                                              dust mite Buroglyphus maynei.";
Int. Arch. Allergy Immunol. 99:180-122 (1992).
-!- FUNCTION: Probable thiol protease.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of mite allergy are bronchial asthma, allergic rhinitis and conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00645; Pept_C1; 1.
PROSITE; PS00640; THIOL PROTEASE ASN; 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
PROSITE; PS00639; THIOL PROTEASE THIS; 1.
Allergen; Glycoprotein; Hydrolase; Protease; Signal; Thiol protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mite group 1 allergen Eur m 1.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
By similarity.
T -> S (in Eur m 1.0102).
M -> I (in Eur m 1.0102).
                                                                                                                      MEDLINE=93130112; PubMed=1483062;
Kent N.A., Hill M.R., Keen J.N., Holland P.W., Hart B.J.;
"Molecular characterisation of group I allergen Eur m I from house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; Length 322.
Pred, No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (Gap).
                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the peptidase C1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 AA.
mite, Euroglyphus maynei.";
Int. Arch. Allergy Immunol. 118:15-22(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF047610; AAC82351.1; -; MRNA.
EMBL; AF047611; AAC82352.1; ALT_INIT; MRNA.
EMBL; AF047612; AAC82353.1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X60073; CAA42677.1; -; Genomic_DNA.
PRI; S21864; S21864.
HSRP; P51634; 1K3B.
MEROPS; C01.073; -.
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. ., IEA.

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Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic insights into methanotrophy: the complete genome sequence of Methylococcus capsulatus (Bath)."; PLOS Biol. 2:1616-1628(2004). EMBL; AE017282; AAU92002.1; -; Genomic_DNA. TIGR; MCA1974; -.
                                                                      "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-1- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
                                                                                                                                                                   TISTALLARALIS BELLOUGH TO LINE GLYCELAIGENYGE-3-PHOSDIALE

Gehydrogenase family.

R FMBL; AE001549; AAD068318.1; -; Genomic_DNA.

R FIRS; C1830; C7130.8

R GO; GO: 0005737; C: Cytoplasm; IEA.

R GO; GO: 0004365; F: Rily binding; IEA.

R GO; GO: 0016491; F: Rily binding; IEA.

R INTERPO: IPR00173; GAPDH-1.

R FRAM; PR00174; GAPDH-1.

R TIGRPAM9; TIGR01244; GAPDH-1.

R TIGRAPAN9; TIGR01244; GAPDH-1.

R TIGR0144; GAPDH-1.

R TIGR0144; GAPDH-1.

R TIGR0144; GAPDH-1.

R TIGR0144; GAPDH-1.

R TIGR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methylococcus capsulatus.
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0003743; F:translation initiation factor activity; IEA. GO; GO:0044249; P:cellular biosynthesis; IEA. InterPro; IPR000649; IF-2B. InterPro; IPR011559; IF-2B_rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 2; Length 330;
Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36003 MW; 2581D417C4112043 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence u
25-0CT-2004 (TrEMBLrel. 28, Last annotation
Initiation factor 2 subunit family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01008; IF-2B; 1.
TIGRFAMB; TIGR00524; eIF-2B_rel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Oxidoreductase
SEQUENCE 330 AA; 36003 MW; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methylococcaceae; Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=MCA1974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q606P2_METCA_PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 HAFKGIVSVD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HSFSGVASVE 10
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=414;
                                                  Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eisen J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q606P2;
                      Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METCA
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Q606P2 MET
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GO: GO:0005137; C:cytoplasm; IEA.
GO: GO:00051287; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.
GO: GO:00051287; F:NAD binding; IEA.
GO: GO:0016491; F:NAD binding; IEA.
GO: GO:0016491; F:Oxidoreductase activity; IEA.
GO: GO:0006006; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR011596; GAPDH-I.
InterPro; IPR011596; GAPDH-I.
PANTHER: PTHR10836; GAP—dhdrogenase.
                                                                                                                                                                                                                                    Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G. Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weigman J.F., Fujil C., Bowman C., Watthey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doig P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
GLYCERALDEHYDB 3-PHOSPHATE DEHYDROGENASE.
Name-gap 2; OrderedLocusNames-JHP1265;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epailonproteobacteria; Campylobacterales;
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MEDLINE-99120557; PubMed-9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
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Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pylori.";
Nature 388:539-547(1997).
-!- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate dehydrogenase family.
EMBL; AE00635; AAD08387.1; -; Genomic_DNA.
PIR; B64688; B64688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome, Oxidoreductase.
SEQUENCE 330 AA; 36021 MW; C5053242B30CBBD5 CRC64;
                                                                                                                                                                                       STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
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IIGRFAMB; TIGR01534; GAPDH-I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF02800; Gp dh C; 1.
Pfam, PF00044; Gp dh N; 1.
PRINTS; PR00078; G3PDHDRGNASE.
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  OrderedLocusNames=HP1346;
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Q9ZJP0;
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264 HAPKGVVSID 273
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01-MAY-1999 (TrEMBLrel.
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                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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TIGR; HP1346; -.
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Best Local Similarity
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                                                                                                              NCBI_TaxID=210;
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Gaps

Length 383;

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Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                 Cryptococcus neoformans var. neoformans B-3501A.
Eukaryota, Fungi, Basidiomycota, Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae, Tremellales; Tremellaceae; Filobasidiella.
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                                                         Gaps
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Pubmed=15576355; DOI=10.1093/nar/gkh970;
Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
Matsui S., Uchiyama I.;
                                                                                                                                                                                                                                                                                                                 Σ
                                                                                                                                                                                                                                                                                                  FUND E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima I Licke B.L., Fu J., Davis R.W.; Subricke B.L., Fu J., Davis R.W.; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 3.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Thermoadaptation trait revealed by the genome sequence of thermophilic Geobacilius kaustophilus.";
Nucleic Acids Res. 32:6292-6303(2004).
EMBL; BA000043; BAD75901.1; -; Genomic_DNA.
                                   Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                  374 AA; 40344 MW; B07E2DE2AC577B1F CRC64;
Complete protecome; Initiation factor.
SEQUENCE 352 AA; 37081 MW; FCB9945B6E6F98F9 CRC64;
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Last annotation update)
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Last annotation update)
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EMBL; AAEY01000028; EAL20539.1; -; Genomic_DNA.
Hypothetical protein.
                                  Score 34; DB 2;
Pred. No. 3e+02;
                                                                                                                                                         374 AA
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                                                        3; Mismatches
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                                  69.4%;
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OrderedLocusNames=GK1616;
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QSKZIS;
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Best Local Similarity 60.0
Matches 6; Conservative
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135 HSFAGVVSL 143
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Best Local Similarity
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SEQUENCE 383 AA
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STRAIN=12822 / ATCC BAA-587;

NUCLECOTIDE SEQUENCE.

STRAIN=12822 / ATCC BAA-587;

MEDLINB=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cordeno-Tarraga A.-M., Temple L., James K.D., Harris B., Ouail M.A.,

Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Relivell T., Goble A., Handin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberzak H., O'Neal S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"And Comparative analysis of the genome sequences of Bordetella pertussis,

"And Comparative Analysis and Bordetella bronchiseptica.";
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EMBL; BX640429; CAE37397.1; -; Genomic_DNA.

EQ): GO:0016021; C:integral to membrane; IEA.

GO; GO:00120289; C:periplasmic space (sensu Gram-negative Bact...

GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006865; P:amino acid transport; IEA.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Putative branched-chain amino acid transporter substrate-binding
                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative branched-chain amino acid transporter substrate-binding
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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OrderedLocusNames=BB1493;
Bordetella bronchiseptica (Alcaligenes bronchisepticus)
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Score 34; DB 2; 1
Pred. No. 3.3e+02;
1; Mismatches 1.
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InterPro; IPR000709; Leu_Ile_Val_bind.
Pfam; PF01094; ANF receptor; 1.
PRINTS; PR00337; LEUILEVALBP.
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   69.4%;
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Q7WM997
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Search completed: April 5, 2006, 17:43:09 Job time : 236 secs

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  T52523
B69406
B69406
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T23013
D25014
A81885
A81885
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A85766
A
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S77206
A97659
AC2883
AD3563
C84552
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T18520
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T30877
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S74361
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AI0638
F81650
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AE0118
T34826
H82955
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A61500
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C69023
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A45565
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B45738
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T26070
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T02197
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JC4037
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 fetuin precursor -
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glyceraldehyde-3-p
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                                                                          2006, 17:39:33 ; Search time 38 Seconds (without alignments) 25.320 Million cell updates/sec
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      5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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       version =
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                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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      GenCore
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Minimum DB Maximum DB

Database

Result No.

Searched:

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A;Molecule type: protein
A;Readudes: 19-56, 'WK, 59-62 <1SH>
A;Readudues: 19-56, 'WK, 59-62 <1SH>
A;Cross-references: UNIPARC: UPI0000177A85
B;Strawich, E.; Glimcher, M.J.
Blur. J. Blochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a A;Reference number: S10780; MUID:90336641; PMID:2379503
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 19-31 cSTR>
A;Cross-references: UNIPARC:UP10000FDE2D
B;Kitajima, K.; Suzuki, T.; Kouchi, Z.; Inoue, S.; Inoue, Y.
Arch. Biochem: Biophys. 319, 393-401, 1995
A;Tile: Identification and distribution of peptide:N-glycanase (PNGase) in mouse org. A;Reference number: S65895; MUID:95305576; PMID:7786020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S22394; S22141
R;Brown, W.M.; Dziegielewska, K.M.; Saunders, N.R.; Christie, D.L.; Nawratil, P.; Mue Bur. J. Blochem. 205, 321-331, 1992
Bur. J. Blochem. 205, 321-331, 1992
A;Title: The nucleotide and deduced amino acid structures of sheep and pig fetuin. Co A;Reference number: S22394; MUID:92209519; PMID:1372866
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A; Residues: 1-364 < PCRN
A; Residues: 1-364 < PCRN
A; Residues: 1-364 < PCRN
C; Superfamily: alpha-2-HS-91ycoprotein; cystatin homology
C; Superfamily: alpha-2-HS-91ycoprotein; cystatin homology
C; Keywords: calcium binding; EF hand; glycoprotein
F; 1-10-Domain: signal sequence #status predicted < SIG>
F; 1-34/Product: fetuin #status predicted < NAT>
F; 23-137/Pomain: cystatin homology < CYL>
                                A;Title: Fetuin and alpha-2HS glycoprotein induce alkaline phosphatase in epiphyseal A;Reference number: A61376; MUID:92084776; PMID:1721070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;146-253/Domain: cystatin homology <CY2>
F;99,156,176/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;146-253/Domain: cystatin homology <CY2>
F;99,156,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule types: protein
A; Residues: 155-159 < KIT>
A; Cross-references: UNIPARC; UP10000177A86
A; Cross-references: UNIPARC; UP10000177A86
C; Superfamily: alpha-2-HS-glycoprotein; cystatin homology
C; Keywords: glycoprotein; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-359/Product: fetuin #status experimental <MAT>F;23-137/Domain: cystatin homology <CXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 2;
Pred. No. 0.1;
1; Mismatches (
       Physiol. 149, 222-234, 1991
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Best Local Similarity 90.v.
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Best Local Similarity 90.0
Matches 9; Conservative
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313 HTFSGVASVE 322
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318 HTFSGVASVE 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetuin precursor - sheep
                                                                                                     A, Accession: A61376
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S10781
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                                                                                                                                                       fetuin precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S22395, S22142
C;Accession: S22395, S22142
Bur. J. Biochem. 205, 321-331, 1992
A;Title: The nucleotide and deduced amino acid structures of sheep and pig fetuin. Common A;Reference number: S22394; MUID:92209519; PMID:1372866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1.362 cBRW>
A;Residues: 1.362 cBRW>
A;Residues: 1.362 cBRW>
A;Residues: 1.362 cBRW>
A;Cross-references: UNIPROT: P29700; UNIPARC: UPI000012501A, EMBL: X56021; NID: g2104; PIDN: C;Superfamily: alpha-2-HS-glycoprotein; cystatin homology
C;Superfamily: alpha-2-HS-glycoprotein; cystatin binding; E; hand; glycoprotein
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-362/Product: feuun #status predicted <MAT>
F;16-362/Product: cystatin homology <CY1>
F;20-134/Domain: cystatin homology <CY2>
F;96,153,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT: P12763; UNIPARC: UP10000125015; CB:X16577; NID: g343; PIDN: CAA
B;Christie, D.L.; Dziegielewska, K.M.; Hill, R.M.; Saunders, N.R.
A;Christie, A4549; 1987
A;Title: Fetuin: the bovine homologue of human alpha-2-HS glycoprotein.
A;Reference number: A26991; MUID: 87190952; PMID: 2436943
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A;Molecule type: protein
A;Molecule type: protein
A;Cross-references: 19-71, 'Q', 73-98, 'X', 100-105,'H', 107-115,'FS',118,'V', 120,'L', 122-123;188-194
A;Cross-references: UNIPARC:UP10000177A81; UNIPARC:UP10000177A82
B;Yet, M.G.; Chin, C.C.O.; Wold, F.
J. Biol. Chem. 263, 111-117, 1988
A;Title: The covalent structure of individual N-linked glycopeptides from ovomucoid and A;Reference number: A29914; MUID:88087074; PMID:2447075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 49; DB 2; Length 362; 100.0%; Pred. No. 0.024; tive 0; Mismatches 0; Indels
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A;Molecule type: protein
A;Residues: 72-103;144-185, P., 187 < YET>
A;Cross-references: UNIPARC:UPI0000177A83; UNIPARC:UPI0000177A84
B;Alcaraz, G; Marti, J; Moinier, D; Fougereau, M.
Biochem. Biophys. Res. Commun. 99, 30-36, 1981
A;Reference number: A05142; MUID:81207262; PMID:6165360
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A;Residues: 19-56,'VK',59-62 <ALC>
A;Cross-references: UNIPARC:UP10000177A85
R;Ishikawa, Y.; Wu, L.N.Y.; Valhmu, W.B.; Wuthier, R.E.
ALIGNMENTS
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Best Local Similarity 100.
Matches 10; Conservative
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Gaps

Gaps

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A;Cross-references: UNIPROT:P97515; UNIPARC:UPI0000125018; DDBJ:D88777; NID:g1688035
                                                                                                                                         A; Molecule type: protein
A; Residues: 19-38 < GOT2>
A; Residues: 19-38 < GOT2>
A; Cross-references: UNITARC: UPI0000177A8B
A; Experimental source: liver
C; Comment: This protein belongs to the fetuin family.
C; Superfamily: alpha-2-HS-glycoprotein; cystatin homology
C; Superfamily: alpha-2-HS-glycoprotein; serine proteinase inhibitor
C; Superfamily: signal sequence #status predicted < SIG>
F; 19-348/Product: countertrypin #status predicted < SIG>
F; 19-348/Product: countertrypin #status predicted < SIG>
F; 11-122/Domain: cystatin homology < CYI>
F; 11-122/Domain: cystatin homology < CYI>
F; 1146-252/Domain: cystatin homology < CYI>
F; 146-252/Domain: cystatin homology < CYI>
F; 19, 156/Binding site: carbohydrate (Asn) (covalent) #status predicted
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8; Conservative
                                                                             A; Experimental source: liver A; Accession: PC4321
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Alpha-2-HS-glycoprotein homolog - mouse

Ny Alternate names: fetuin homolog; fetuin type trypsin inhibitor countertrypin

C; Species: Mus musculus (house mouse)

C; Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004

C; Accession: S21094; D47408; A47408; E47408

R; Yang, F; Chen, Z.L.; Bergeror, J.M.; Cupples, R.L.; Friedrichs, W.E.

Biochim. Biophys. Acta 1130, 149-156, 1992

A; Title: Human alpha(2)-HS-glycoprotein/bovine fetuin homologue in mice: identification

A; Reference number: S21094; MUID: 92223088; PMID: 1373325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Countertrypin precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 17-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5431; P4321
R;Goto, K.; Yoshida, K.; Suuki, Y.; Yamamoto, K.; Sinohara, H.
J. Biochem. 121, 619-625, 1997
A;Title: Molecular cloning and sequencing of cDNA encoding plasma countertrypin, a membe A;Reference number: JC5431; MUID:97279057; PMID:9133634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: UNIPROT:P29699; UNIPARC:UPI00000191F; GB:S96534; NID:g248763; PIDN: R;Yamamoto, K.; Sinohara, H. B. D. Biol. Chem. 268, 17750-17753, 1993
A;Title: Isolation and characterization of mouse countertrypin, a new trypsin inhibitor A;Reference number: A47408; MUID:93352581; PMID:7688730
A;Accession: D47408
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A/Experimental source: plasma
A/Note: sequence extracted from NCB1 backbone (NCBIP:136437)
A/Accession: A47408
A/Accession: A47408
A/Status: preliminary
A/Accession: B47408
A/Experimental source: plasma
A/Note: sequence extracted from NCBI backbone (NCBIP:136431)
A/Accession: B47408
A/Accession: B47408
A/Accession: B1-98, L',100-101, I',103-105 <YA3>
A/Accession: B1-98, L',100-101, I',103-105 <YA3>
A/Accession: B1-98, L',100-101, I',103-105 <YA3>
A/Accession: C47408
A/Accession: 
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A,Status: preliminary
A,Molecule type: protein
A,Rolecules: 276-295 < xAM>
A,Residuss: 276-295 < xAM>
A,Cross-references: UNIPARC:UPI0000177A87
A,Experimental source: plasma
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-345 < vAN>
A, Cross-references: UNIPR
R, Yamamoto, K.; Sinohara,
J. Biol. Chem. 268, 17750
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A; Molecule type: mRNA
A; Residues: 1-348 <GOT1>
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Matches
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fetuin precursor - rat

N.Alternate names: 59% bone sialoprotein; tyrosine kinase inhibitor

N.Alternate names: 59% bone sialoprotein; tyrosine kinase inhibitor

Species: Rattus norvegicus (Norway rat)

C.Bate: 12-Oct-1389 #sequence revision 12-Oct-1989 #text_change 09-Jul-2004

C.Accession: A32827; S22382; I55489; A40766; A33144

R.Auberger, P.; Palquerho, L.; Contreres, J.O.; Pages, G.; Le Cam, G.; Rossi, B.; Le

Call 58, 631-640, 1989

A.Title: Characterization of a natural inhibitor of the insulin receptor tyrosine ki:

A.Reference number: A32827; MUID:89354538; PMID:2766355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 18-62, 'D', 64-92,'E', 94-287,'A', 289-353,'GPVA',358,'LCP',362,'RVRYFKI' <R', A;Cross-references: UNIPARC:UP1000012501C; EMBL:X63446; NID:956139; PIDN:CAA45042.1; R;Ohnishi, T.; Nakamura, O.; Ozawa, M.; Arakaki, N.; Muramatsu, T.; Daikuhara, Y. J. Bone Miner. Res. 8, 36-377, 1993
A;Title: Molecular cloning and sequence analysis of cDNA for a 59 kD bone sialoprote: A;Reference number: 155489; MUID:93206661; PMID:7681247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 18-62, U', 18-7, 94-287, 'A', 289-353, 'GPVA', 358, 'LCP', 362, 'RVRYFKI' <R1
A;Residues: 18-62, U', 16-492, 'E', 94-287, 'A', 289-353, 'GPVA', 358, 'LCP', 362, 'RVRYFKI' <R1
A;Cross-references: UNIPARC:UP1000012501C; GB:D10261; NID:9220675; PIDN:BAA01101.1; I
R;Ohnishi, T.; Arakaki, N.; Nakamura, O.; Hirono, S.; Daikuhara, Y.
J. Blol. Chem. 266, 14636-14645, 1991
A;Title: Purification, characterization, and studies on biosynthesis of a 59-kDa bone be the rat counterpart of human alpha-2-H8 Glycoprotein and is synthesized by both he A;Reference number: A40766; MUID:91317830; PMID:1860865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 36, 'XE', 39-44, 'XQ', 47-48, 'XNN', 52,'X', 69-82;183-192,'X', 194-198;249-252,'
A,Roseidues: 26, 'XE', 39-44, 'XQ', 47-48, 'XNN', 52,'X', 69-82;183-192,'X', 194-198;249-252,'
A,Croseizences: UNIPARC:UPI0000177A7C; UNIPARC:UPI00001777
C;Superfamily: alpha-2-HS-glycoprotein; cystatin homology
C;Superfamily: alpha-2-48-glycoprotein; cystatin homology
C;Y153-269/Domain: cystatin homology c(Y1>
F;163-269/Domain: cystatin homology c(Y2>
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A;Residues: 1-375 <AUB>
A;Residues: 1-375 <AUB>
A;Crose conservation of the conserva
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37964
S;DevLin, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: 221757
A;Accession: T37964
A;Accession: T37964
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3227 <DBV>
A;Residues: 1-3227 <DBV>
A;Experimental source: Strain 972h-; Cosmid C19D5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72628
R;Kawarabayasi, Y; Hino, Y; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. Jilitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cysteine proteinase (EC 3.4.22.-) - Euroglyphus maynei
NiAlternate names: allergen Eur m I
C.Species: Buroglyphus maynei
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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A;Cross-references: UNIPROT:P25780; UNIPARC:UP1000016BEC4; EMBL:X60073
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R;Kent, N.A.; Hill, M.; Keen, J.N.; Holland, P.W.H.; Hart, submitted to the EMBL Data Library, June 1991
A;Reference number: S21864
                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 2; I
Pred. No. 2.1e+02;
1; Mismatches 1;
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C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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125 SFSGIASI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HSFSGVAS 8
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A,Status: preliminary
A,Molecule type: DNA
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A,Status: preliminary
A,Molecule type: DNA
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A;Residues: 1-215 <STO>
A;Cross-references: UNIPROT:Q9HXV4; UNIPARC:UPIO00012DBDF; GB:AE004788; GB:AE004091; NIC
A;Experimental source: strain PAO1
C;Genetics:
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A.Description: P560/270 expressed in embryonic abdominal leg cells of Bombyx mori can tr
A;Reference number: Z18815
A;Accession: T18200
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A;Molecule type: mRNA
A;Residues: 1-2342 <UEN
A;Residues: 1-2342 <UEN
A;Cross-references: UNIPROT:O01677; UNIPARC:UPI00000827E4; EMBL:U67866; NID:g2058457; PI
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-{acyl-carrier-protein} synthase I home
ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-
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C;Species: Bombyx mori (silkworm)
C;Accession: T18200
C;Accession: T18200
R;Ueno, K.
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probable ubiquitin ligase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
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Pred. No. 7.2;
                                                              Length 375
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                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                            Score 38; DB 2;
Pred. No. 4.9;
1; Mismatches
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                                                         77.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%;
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C,Superfamily: adenylate kinase
                                                                                   Best Local Similarity 80.0
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.5
Best Local Similarity 70.0
Matches 7; Conservative
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323 HAFSPVASVE 332
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195 HSIAGVGSVE 204
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583 HSFVGIAAVQ 592
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tes 6; Conserv
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A;Status: preliminary
                                                              Query Match
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Matches
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69.4%;
50.0%;
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Best Local Similarity 50.00,
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264 HAFKGVVSID 273
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264 HAFKGIVSVD 273
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                                                                                                                                                                                                                                                                                                         phosphoprotein phosphatase (EC 3.1.3.16) 1 F25B3.4 [similarity] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004 R;Gardher, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 5
A; Map position: 5
A; Introns: 20/2; 157/3; 273/3
C; Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phose C; Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specif F; 7-268/Domain: phosphoprotein phosphatase homology <PRC>
F; 35-103/Domain: phosphoesterase core homology <PRC>
F; 41.43, 69/Binding site: iron (Asp. His, Asp) #status predicted
F; 69, 101, 151, 227/Binding site: iron (Asp. Asn. His, His) #status predicted
F; 72, 102, 251/Active site: Asp, His, Tyr #status predicted
F; 73, 200/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-291 cWILD:
A;Cross-references: UNIPROT:Q27496; UNIPARC:UP1000007D589; EMBL:Z70752; PIDN:CAA94756.1;
A;Experimental source: clone F25B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Helicobacter Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
CiAccession: B64688
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Accession: B64688
A;Status: praliminary; nucleic acid sequence not shown; translation not shown
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A/Residues: 1-330 <TOM>
A/Cross-references: UNIPROT:025902, UNIPARC:UPI0000003154; GB:AE000635, GB:AE000511; NID
C/Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C/Keywords: glycolysis; NAD; oxidoreductase
F;149,176/Active site: Cys, His #status predicted
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                                      Length 211;
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                                                                                       Indels
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                                   2,
                             Score 34; DB
Pred. No. 18;
1; Mismatches
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submitted to the EMBL Data Library, April 1996
A'Reference number: 219406
A'Accession: T21322
                        69.4%;
                                                                               Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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37 AFSGVASTE 45
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                                                                                                                             2 SFSGVASVE 10
Ouery Match
Best Local Similarity
7; Conserve
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Glyceraldehyde 3-phosphate dehydrogenase - Helicobacter pylori (strain J99)
Clybecies: Helicobacter pylori
Clybecies: Helicobacter pylori
Clybecies: 12-Feb-1999
#sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
Clybecession: C71830
Clyber: 12-Feb-1999
#sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
Clybecession: C71830
Nature 397, 176-180, 1999
Nature 397
Nature 397
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A;Cross-references: UNIPROT:Q9ZJPO; UNIPARC:UPI00000D3719; GB:AE001549; GB:AE001439;
A;Experimental source: strain J99
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A;Cross-references: UNIPROT:Q9XTE4; UNIPARC:UPI00007EF8B; EMBL:Z82260; PIDN:CAB0514;
A;Experimental source: clone C32H11
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T3450
T23450
R;Barlow, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19157
A;Accession: T19652
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 96/2; 134/1; 184/1; 239/1; 290/3; 311/2; 348/1; 419/2
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A;Gens: gap 2
C;SuperfamilTy: glyceraldehyde-3-phosphate dehydrogenase
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A;Molecule type: DNA
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Pred. No. 30;
3; Mismatches
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A,Accession: S03380
A,Status: preliminary
A,Molecule type: protein.
A,Molecule type: protein.
A,Residues: 1-28;29-43;44-60;61-76;77-94 <SIM>
A,Residues: US8;29-43;44-60;61-76;77-94 <SIM>
C,COSB-references: UNIPROT:Q/M431; UNIPARC:UPI000002F520; UNIPARC:UPI0000175D1D; UNI
C,Superfamily: papain
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam Ster, E.W.
A;Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Status: preliminary
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A,Cross-references: UNIPROT:Q8UHC3; UNIPARC:UPI0000D1901; GB:AE008688; PIDN:AAL41775
A,Experimental source: strain C58 (Dupont)
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A;Molecule type: DNA
A;Residues: 1-128 <-PAU>
A;Cessidues: 1-128 <-PAU>
A;Cross-references: UNIPROF:Q19063; UNIPARC:UPI0000077294; EMBL:UZ8943; NID:g861333;
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein E04F6.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15911
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                                                                                                                                                                                                                  Score 33; DB 2
Pred. No. 13;
2; Mismatches
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                                                                                                                                                                                                                     67.3%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
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A;Introns: 29/3; 104/3
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A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: Nostoc sp. strain PCC 7120
C;Accession: AB2457
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sp. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840
A;Retus; Preliminary
A;Accession: AB2457
A;Status; Preliminary
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N;Alternate names: allergen Der pl
C;Species: Dermatophagoides pteronyssinus
C;Species: Dermatophagoides pteronyssinus
C;Date: 05-Mar-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S03380
C;Accession: N.J.; Nice, B.C.; Moritz, R.L.; Stewart, G.A.
Protein Seq. Data Anal. 2, 17-21, 1989
Protein Seq. Data Anal. 2, 17-21, 1989
A;Title: Structural studies on the allergen Der pl from the house dust mite Dermatophagof A;Reference number: A31657; MUID:89098855; PMID:2911558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1558 <KUR>
A; Cross-references: UNIPROT: QBYLT6; UNIPARC: UPI00000CEDCF; GB: BA000019; PIDN: BAB76909.1;
A; Experimental source: strain PCC 7120
                                                Deta-galactosidase (EC 3.2.1.23) II precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04440
R;Smith, D.L.; Starrett, D.A.; Gross, K.C.
Plant Physiol. 117, 417-423, 1998
A;Title: A gene coding for tomato fruit beta-galactosidase II is expressed during fruit A;Reference number: Z15296; MUID:98289087; PMID:9625694
A;Accession: T04340
                                                                                                                                                                                                                                                                                                      A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.FOLOUIE type: mRNA
A.Residues: 1-724 <SMI>
A.Coss-references: UNIPROT: 081100; UNIPARC: UPI00000AC774; EMBL:AF020390; NID:g3299895;
A.Experimental source: strain Rutgers; tissue-type tomato fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Kerwords: glycosidase; hydrolase -
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-724/Product: beta-galactosidase II #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.4%; Score 34; DB 2; Length 724; llarity 70.0%; Pred. No. 68; Conservative 1; Mismatches 2; Indels
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C,Superfamily: beta-galactosidase bga
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Best Local Similarity 60.0
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594 HSLSGSSSVE 603
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153 HNYRGVASAE 162
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les 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-258 <STO>
A;Residues: 1-258 <STO>
A;Cross references: UNIPROT:09X6P4; UNIPARC:UPI000012E8B4; GB:AE004784; GB:AE004091.
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: lpxA; PA1644
C;Superfamily: acyl-(acyl-carrier-protein):UDP-N-acetylglucosamine O-acyltransferase
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A;Cross-references: UNIPROT:P77793; UNIPARC:UPI000013A946; GB:BA000007; PIDN:BAB3551
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein EC82095 [imported] - Escherichia coli (strain O157:H7, substrain Cispecies: Escherichia coli (species: Escherichia coli (speciesion: G9089)

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, A;Hayashi, T.; Makino, K.; Ohnishi, M.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Retus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Escherichia coli (strain O157:H7, substrai
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A,Experimental source: strain O157:H7, substrain EDL933
C,Genetics:
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85727
A;Accession: B85727
A;Residues: 1-460 <STO>
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66.7%; Pred. No. 68;
iive 1; Mismatches
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Pred. No. 68;
1; Mismatches
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Similarity 75.0%;
6; Conservative :
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227 HYFSGIAEV 235
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164 HSFSGMGS 171
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Best Local Similarity
Matches 6; Conserva
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G97451
G97651
G97661
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <KUR>
A;Cross-references: UNIPROT:Q8UHC3; UNIPARC:UPI0000D1901; GB:AE007869; PIDN:AAK86568.1;
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A;Molecule type: DNA
A;Residues: 1-150 <ZIM>
A;Cross-references: UNIPROT:P26943; UNIPARC:UPI000013C156; EMBL:X57853; NID:g48840; PIDN
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UDP-N-acetylglucosamine acyltransferase PA3644 [imported] - Pseudomonas aeruginosa (stracispecies: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: DB3190
C;Accession: DB3190
C;Accession: DB3190
C;Accession: DB3190
C;Accession: DB3190
C;Accession: DB3190
M.Y. Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
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60.0%; Pred. No. 21;
tive 2; Mismatches 2; Indels
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Best Local Similarity 60.0
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                                                                   HSFEGVAA 128
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HSFSGVAS 8
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2; Indels

us-10-772-537-4.rpr

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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Recence number: A86141; MUID:21016719; PMID:11130712

A; Residues: 1-890 & CSTO-

A; Residues: 1-890 & CSTO-

A; Residues: 1-890 & CSTO-

A; Cross-references: UNIPROT:Q9LQ11; UNIPARC:UP100000483E9; GB:AE005173; NID:g8493583; C; Genetics:

C; Genetics:
C; Superfamily: Receptor-like protein kinase
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C;Date: 20-0ct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52523
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatı
submitted to the Protein Sequence Database, September 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1209 <SCH>
A;Cross-references: UNIPROT:Q9FF13; UNIPARC:UP1000017B49A; EMBL;AL442164; GSPDB:GN00:
A;Experimental source: BAC clone B2J23; strain OR74A
C;Genetics:
A;Gene: NCSP:B2J23.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:083728; UNIPARC:UPI0000131DB6; GB:AE001246; GB:AE000520; A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable pyruvate, phosphate dikinase - syphilis spirochete ('Species: Treponema pallidum subsp. pallidum (syphilis spirochete) ('Date: 24-Jul-1998 #text_change 09-Jul-2004 ('Accession: G71286 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 ('Accession: G71286 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 ('Accession: G71286 'A. Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R. Fraser, C.M.; Norris, S.J.; Weinstock, J. Kowell, J.K.; Chidambaram, M.; Utterback, T they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. (A. Chidambaram, M.; Utterback, T A. Science 281, 375-388 1998 (A. MUD:98332770; PMID:965876 A. A. Stetence number: A71250; MUD:98332770; PMID:965876 A. A. Stetus: preliminary; nucleic acid sequence not shown; translation not shown A. Stesiques: 1-901 (COL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B2J23.190 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: TP0746
C,Superfamily: pyruvate, phosphate dikinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
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251 NSFDGVASFE 260
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720 HAYQGIGSIE 729
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Best Local Similarity
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nes 7; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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Best Local S
Matches 7
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                                                                                                         hypothetical protein b1490 - Escherichia coli (etrain K-12)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Accession: E64902
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Accession: E64903
A;Title: The complete genome sequence of scherichia coli K-12.
A;Accession: E64902
A;Refatus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-460 <BLAT>
A;Croses-references: UNIPROT:P7793; UNIPARC:UPI000013A946; GB:AE000246; GB:U00096; NID:GA;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Bacillus pumilus
Cispecies: Bacillus pumilus
Cibate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CiAccession: 519729
R;Xu, W.Z.; Shima, Y.; Negoro, S.; Urabe, I.
Bur. J. Biochem. 202, 1197-1203, 1991
A;Title: Sequence and properties of beta-xylosidase from Bacillus pumilus IPO. Contradic
A;Reference number: 519729; MUID:92111496; PMID:1765080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-535 <XUW>
A;Residues: 1-535 <XUW>
A;Cross-references: UNIPROT:P07129; UNIPARC:UPI000013908B; EMBL:X05793; NID:g48663; PIDN
A;Experimental source: strain IPO
C;Genetics:
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin C.W.; Chwig, M.K.; Comm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Ransen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
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A;Start codon: TTG
C;Function:
A;Description: hydrolysis of 1,4-beta-D-xylan
A;Pathway: xylan degradation
C;Superfamily: Xylan 1,4-beta-xylosidase (EC 3.2.1.37)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Length 460;
Pred. No. 68;
1; Mismatches 2; Indels
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Pred. No. 80;
2; Mismatches 2; Indels
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peroxidase ATP21a - Arabidopsis thaliana
N.Alternate names: protein F3A4.40
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 04-Peb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C.Accession: T45849
R.Bargues, M.: Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; submitted to the Protein Sequence Database, December 1999
A.Reference number: Z23007
A.Reference pression: T45849
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-329 cara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31121
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT: 085830; UNIPARC: UPI000005C952; EMBL: AF079317; NID: 933782
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C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23013
R;Lennard, N.
R;Lennard, N.
R;Reference number: Z19653
A;Recession: T23013
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                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q96510; UNIPARC:UPI0000048820; EMBL:AL132978
A;Experimental source: cultivar Columbia; BAC clone F3A4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.3%; Score 32; DB 2; Length 329; Best Local Similarity 50.0%; Pred. No. 77; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
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A;Molecule type: DNA
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A;Residues: 1-417 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%; Score 32; DB 77.8%; Pred. No. 94; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Superfamily: bicyclomycin resistance protein
                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3
A;Introns: 72/3; 139/3; 195/1
A;Note: F3A4.40
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Matches 7; Conservative
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T31121
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T23013
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                                                                                                                                                                                                                                                                                                                probable 3-isopropylmalate dehydratase - Archaeoglobus fulgidus

N;Alternate names: conserved hypothetical protein AF1251

C;Species Archaeoglobus fulgidus

C;Species Archaeoglobus fulgidus

C;Bete: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: B69406

R;Klenk, H. P; Clayton, R. A; Tomb, J.F; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

S; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Karkness, E.P.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

N,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Accession: B69406

A; Reference number: A69250; MUID:98049343; PMID:9389475

A; Reference number: A69250; MUID:98049343; PMID:9389475

A; Residues: preliminary; nucleic acid sequence not shown; translation not shown

A; Residues: 1-239 eXLES

A; Cross-references: UNIPROT:029017; UNIPARC:UPI0000056DD6; GB:AE001018; GB:AE000782; NID

C; Superfamily: 3-isopropylmalate dehydratase leub chain
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0
                                                                 67.3%; Score 33; DB 2; Length 1209; 60.0%; Pred. No. 1.9e+02; 1.0 i. Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.3%; Score 32; DB 1; Length 239; 60.0%; Pred. No. 55; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%; Score 32; DB 2; Length 257; llarity 85.7%; Pred. No. 59; Conservative 0; Mismatches 1; Indels
A;Map position: 6
A;Introns: 206/2; 752/1; 896/3
                                                                                                                  Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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113 YSFAGVATFE 122
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                                                               Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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G86710
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 31-Dec-2004
C;Accession: B62444
R;Heidelberg, J.R.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. R;Heidelberg, J.R.; Expolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers chardson, D.; Ermolaeva, M.D.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 31-Dec-2004
C;Accession: A81885
R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491
A;Reference number: A81885
A;Accession: A81885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: pntB; NMA1175
C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-spe
C;Keywords: oxidoreductase
F;21-459/Domain: NAD(P)+ transhydrogenase (B-specific) beta chain homology <TBB>
                                                                                                                                                                                                                                                                                                                                                                                                                                NAD(P) transhydrogenase, beta chain VCA0564 [imported] - Vibrio cholerae (strain N169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 2
C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-458 <HEI>
A;Cross-references: UNIPROT:Q9KM25; UNIPARC:UPI0000C3583; GB:AE004387; GB:AE003853;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/STATUS: DEFINATION A/MOLECULE TYPINATE BY A/REGIQUES: 1-461 <PAR>
A/REGIQUES: 1-461 <PAR>
A/REGIQUES: 1-461 <PAR>
A/CROSS-references: UNIPROT:09JURS; UNIPARC:UPI00000C4B2F; GB:AL162755; GB:AL157959;
A/Experimental source: serogroup A, strain 22491
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                                                                                                           Score 32, DB 2, Length 455
Pred, No. 1.1e+02;
2, Mismatches 2, Indels
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66.7%; Pred. No. 1.18+02;
ive 2; Mismatches 1; Indels
A;Experimental source: adult testis; clone DKFZp434C0917
C;Genetics:
A;Note: DKFZp434C0917.1
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Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1;
                                                                                                           65.3%;
ilarity 60.0%;
Conservative
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91 HSFVGMAAV 99
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                                                                                                        Query Match
Best Local Similarity
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Matches 6, Conserv
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A;Molecule type: DNA
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A; Experimental source: strain 935c

A; Experimental source: strain 935c

R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fronca, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laight chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.R.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Siva, Santelli, R.V.; Sawasak A; Ruthors: da Silva, A.C.R.; da Silva, R.M.; Silva Jr., W.A.; da Silva, R.C.; Palmieri, D. A; Contents: annotation

C; Genetics: annotation

C; Genetics: A.G. Superfamily: phosphoribosylamine-glycine ligase ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispacesion: T42670
Ribloccker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, November 1999
A;Reference number: Z22230
A;Reference number: Z22230
A;Reference protein T42670
A;Status: preliminary
A;Rolecule 'Ype: mRNA
A;Residues: 1-455 <AAA>
A;Residues: 1-455 <AAA>
A;Coss-references: UNIPROT:Q9UW8; UNIPARC:UPI000006DB0A; EMBL:AL133070
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Pred. No: le+02;
4; Mismatches 0; Indels
                                                                                                                                                                    Score 32; DB 2; Length 417;
Pred. No. 99;
1; Mismatches 1; Indels
                    C;Genetics:
A;Gene: CESP:F59F5.1
A;Map position: X
A;Introns: 2/3; 38/1; 85/1; 135/3; 178/3; 217/2; 244/3; 286/1
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A; Experimental source: clone F59F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 55.6%;
5; Conservative
                                                                                                                                                                 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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344 HNFSGFAS 351
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Matches 5; Conserv
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Matches 6; Conservative
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91 HSFVGLAAV 99
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C;Keywords: oxidoreductase
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R; Ahmad, S.; Glavas, N.A.; Bragg, P.D.

Bur. J. Biochem. 207, 733-739, 192

A; Title: A mutation at Gly314 of the beta subunit of the Escherichia coli pyridine nucle A; Reference number: S24380; MUID:92339464; PMID:1633824

A; Residues: 1-462 AAMA

A; Residues: 1-462 AAMA

A; Residues: 1-462 AAMA

A; Residues: 1-462 AAMA

A; Coss-references: UNIPROT: P07002; UNIPARC:UP10000131D63; EMBL:X66086; NID:942455; PIDN R; Closs-reference number: A91172; MUID:86274751; PMID:3525165

A; Molecule type: DNA

A; Residues: 1-220, ABLVIRIGGGCGCGIYAQQRPV', 242-462 ACIA>
A; Residues: 1-220, ABLVIRIGGCGCGIYAQQRPV', 242-462 ACIA>
A; Residues: 1-220, ABLVIRIGGCGCGIYAQQRPV', 242-462 ACIA>
A; Reference number: A91172; MUID:86274751; PMID:3525165

A; Molecule type: DNA

A; Residues: 1-220, ABLVIRIGGCGCGIYAQQRPV', 242-462 ACIA>
A; Reference number: A91172; MUID:92031646; PMID:1932078

A; Tong, R.C. W; Glavas, N.A.; Bragg, P.D.
Biochim: Biophys: Acta 1080, 19-28, 1991

A; Title: Topological analysis of the pyridine nucleotide transhydrogenase of Escherichia A; Reference number: S18355; MUID:92031646; PMID:1932078
                                                                                                                                                                                                                                                                                                                           Rifetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.B. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; r., H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, D.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUID:20178755; PMID:10710307
A;Status: preliminary
A;Residues: 1-461 <FT>
A;Residues: 1-461 <FT>
A;Residues: 1-461 <FT>
C;Genetics: GENEROLOGIOUS B, Strain MCS8
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C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-specif
F;21-459/Domain: NAD(P)+ transhydrogenase (B-specific) beta chain homology <TBB>
                                                                                                                                                                                          NAD(P) transhydrogenase, beta chain NMB0978 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2004
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A;Readdues: 266-277;364-373 <TON>
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
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A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
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|HSFVGLAAV 99
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91 HSFVGLAAV 99
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                                                                                                                                                                                                                                                                                                      C; Accession: C81137
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A Pathway: NAD phosphorylation and dephosphorylation (Sybperfamily: NAD(P) transhydrogenase (B-sp (Sybperfamily: NAD(P) transhydrogenase, beta subunit; NAD(P) + transhydrogenase (B-sp (SKeywords: heterotetramer; inner membrane; transmembrane protein; NAD; NADP; oxidor P;5-21/Domain: transmembrane #status predicted <PML> F;21-62/Domain: NAD(P) + transhydrogenase (B-specific) beta chain homology <PBB> P;36-52/Domain: transmembrane #status predicted <PML> P;50-75/Domain: transmembrane #status predicted <PML> P;86-102/Domain: transmembrane #status predicted <PML> P;444>
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C; Species: Salmonella enterica subsp. enterica servar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 31-Dec-2004
C;Accession: A10682
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Retus: preliminary
A;Molecule type: DNA
A; A. Constant A. C. A. Davie
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NAD(P) transhydrogenase (B-specific) (EC 1.6.1.1) beta chain - Escherichia coli (str:
C;Species: Escherichia coli
                                                                                                                                       A;Cross-references: UNIPARC:UP10000131D63; GB:AE000255; GB:U00096; NID:g178785; PII A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: catalyzes the reversible hydride ion transfer between NAD and NADP; t
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A;Cross-references: UNIPARC:UPI000059E72; GB:AL513382; PIDN:CAD01834.1; PID:g165026
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A,Status: nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                     A;Map position: 35 min \underline{C}_{1}Complex: heterotetramer; two alpha and two beta chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F)125-141/Domain: transmembrane #status predicted <TM5>
F)163-179/Domain: transmembrane #status predicted <TM6>
F)184-200/Domain: transmembrane #status predicted <TM7>
F)205-221/Domain: transmembrane #status predicted <TM7>
F)240-256/Domain: transmembrane #status predicted <TM9>
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66.7%; Pred. No. 1.1e+02;
iive 2; Mismatches 1;
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us-10-772-537-4.rpr

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Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 7
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Best Local Similarity 66.77
Matches 6; Conservative
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91 HSFVGLAAV 99
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NAD(P) transhydrogenase (B-specific) (EC 1.6.1.1) beta chain - Escherichia coli (strain C) Species: Escherichia coli (strain C) Species: Escherichia coli (strain C) Species: Escherichia coli (c) Species: Ba-Uul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C; Accession: D90917
R; Hayasahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasuunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-462 <HXY>
A; Residues: 1-462 <HXY>
A; Residues: 1-462 <HXY>
A; Residues: 1-462 <HXY>
A; Coperences: UNIPROT:P07002; UNIPARC:UP10000131D63; GB:BA000007; PIDN:BAB35731.1; A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: C; Steywords: oxidoreductase
                           C) Accession: A85766
R) Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A885480; MUD:21074935; PMID:11206551
A; Reference number: A885480; MUD:21074935; PMID:11206551
A; Reference number: A885480; MUD:21074935; PMID:11206551
A; Reference: DNA
A; Residues: 1-462 < STO>
A; Residues: 1-462 < STO>
A; Residues: 1-462 < STO>
A; Cross-references: UNIPROT: P07002; UNIPARC:UP10000131D63; GB:AE005174; NID:912515580; FA; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
C; Genetics:
C; Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P) + transhydrogenase (B-specif C; Keywords: oxidoreductase
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Cibate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
Cibate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
Cibate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
Cibate: 02-Nov-2001
Cibate: 02-Nov-2001
Cibate: 02-Nov-2001
Cibate: 03-Nov-2001
Cibate: 03-
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NAD(P) transhydrogenase (AB-specific) (EC 1.6.1.2) - Yersinia pestis (strain C092)
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C; Date: 16-Feb-2001 #Bequence_revision 16-Feb-2001 #text_change 31-Dec-2004
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66.7%; Pred. No. 1.1e+02;
iive 2; Mismatches 1; Indels
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ilarity 66.7%; Pred. No. 1.1e+02;
Conservative 2; Mismatches 1;
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Best Local Similarity 66.7
Matches 6; Conservative
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91 HSFVGLAAV 99
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A;Cross-references: UNIPROT:Q8ZE80; UNIPARC:UPI0000DCCFC; GB:AL590842; PIDN:CAC91107
C;Genetics:
A;Gene: parts
C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-spe
C;Keywords: oxidoreductase
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A;Experimental source: strain Madrid E
C;Genetics:
A;Genetics:
C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P) + transhydrogenase (B-spe
P;21-462/Domain: NAD(P) + transhydrogenase (B-specific) beta chain homology <TBB>
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A;Status: preliminary
A;Nolecule type: DNA
A;Rosidues: 1-465 «KUR»
A;Cross-references: UNIPROT:Q92JG3; UNIPARC:UPI0000CBCA7; GB:AE006914; PIDN:AAL02642
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C,Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-spe
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C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Bickettsia conorii
C;Species: Bickettsia conorii
C;Species: Bickettsia conorii By7112
R;Ogata, H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Brolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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HSFVGLAAV 103
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A.; Liu, F.; Wollam, C. Science 294, 2323-2328,
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A,Residues: 1-474 <TIGNS
A;Cross-references UNIPRO
C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-specif
C;Keywords: heterodimer; membrane protein; NAD; oxidoreductase
F;21-474/Domain: NAD(P)+ transhydrogenase (B-specific) beta chain homology <TBB>
                                                                                         <u>u</u>
                                                                                         C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 31-Dec-2004
R.P. Beandon, R.D.; Paince, D.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, Science 269, 496-512, 1995
A.Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.Reference number: A64000; WUID:95350630; PMID:7542800
A.Accession: F64119
A.Accession: F64119
A.Statues nucleic acid sequence not shown; translation not shown
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C;Accession: S77206
R;Kaneko, T; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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C;Superfamily: NAD(P) transhydrogenase, beta subunit; NAD(P)+ transhydrogenase (B-specif
C;Keywords: NAD; NADP; oxidoreductase
F;21-464/Domain: NAD(P)+ transhydrogenase (B-specific) beta chain homology <TBB>
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                                                                    NAD(P) transhydrogenase (B-specific) (EC 1.6.1.1) beta chain - Haemophilus influenzae
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A;Staturs: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-480 <KAN>
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Alfitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97159; MUID:21608551; PMID:11743194
A; Reference number: A97559
A; Status: preliminary
A; Status: preliminary
A; Rolecule type: DNA
A; Residues: 1-481 «KUR>
A; Residues: 1-481 «KUR>
A; Compassion of the Compassi
C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
3, 2001
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.	using sw model	17:55:39 ; Search time 24 Seconds (without alignments) 12.997 Million cell updates/s	10	Gapext 0.5	31191982 residues	chosen parameters:	. 0000	n 0% n 100%	E 100 summaries	oplications AA New:* odata1/pubpaa/US08 NEW PUB.pep:*	Jaces 1, Tubpas 1980 - New Pub. pep: * ddata/1/pubpas/1807 NEW Pub. pep: * ddata/1/pubpas/PCT_NEW Pub. pep: *	odata//pubpaa/USO9 NEW PUB.pep:* odata//pubpaa/USIO_NEW_PUB.pep:* odata//pubpaa/USI1 NEW PUB.pep:*	odata/1/pubpaa/US60_NEW_PUB.pep:*	results predicted by chance to have a to the score of the result being printe	of the total score distribution.	SUMARIES	B ID Descripti	US-10-764-945-4 Sequence 4.	US-11-178-143-4 Sequence 4, US-10-764-945-1 Sequence 1	US-10-764-945-5 Sequence 5,	US-11-178-143-1 Sequence 6, US-11-178-143-1 Sequence 1,	US-11-178-143-5 Sequence 5, US-11-178-143-6 Sequence 5	US-10-888-962-5 Sequence 5, IIS-10-764-945-7	US-11-178-143-7 Sequence 7, 116-178-143-7	US-10-888-962-7, Sequence 7, US-10-888-962-8 Sequence 8,	US-11-112-882-4 Sequence 4,	US-11-096-568A-5071 Sequence 507	US-11-096-568A-5070 Sequence 5070, US-10-498-026-107	US-10-498-026-109 Sequence 108,	US-11-146-428-110 Sequence 110, US-11-096-568A-6477 Sequence 6477,	US-11-096-568A-6476 Sequence 6476,	equence 6475, equence 6794, equence 109,	
ഗമ	search, using sw	5, 2006, 17:55:39 ; Search time 24 Seconds (without alignments) 12.997 Million cell updates/s	, ,	, Gapext 0.	31191982	satisfying chosen parameters:	gth: 0 gth: 2000000000	Match	isting first 100 summaries	ublished Applications AA_New: * /SIDSST/prodate///pubpad/pub/pad/min.applications/mood.num.applications/mood.n	/SIDSS/ptodata/1/pubpaa/VSO7 NEW PUB.pep:* /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pep:* /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pep:*	/sluss/prodara/1/pubpaa/USO9_NEW_PUB.pep:* /SlDSs/prodara/1/pubpaa/USO_NEW_PUB.pep:* /SlDSs/ptodara/1/pubpaa/USO1_NEW_PUB.pep:*	/SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*	umber of results predicted by chance to have a or equal to the score of the result heing wrinter	analysis of the total score distribution.	SUMMARIES	Length DB ID Descripti	.0 10 6 US-10-764-945-4 Sequence 4.	.0 10 7 US-11-178-143-4 Sequence 4, .9 10 6 US-10-764-945-1 Sequence 1,	.9 10 6 US-10-764-945-5 Sequence 5,	.9 10 b US-1U-/64-945-6 Sequence 6, .9 10 7 US-11-178-143-1 Sequence 1,	.9 10 7 US-11-178-143-5 Sequence 5, .9 10 7 US-11-178-143-6 Sequence 5	.9 359 6 US-10-888-962-5 Sequence 5,	6 10 7 US-11-178-143-7 Sequence 7, Sequence 7, Sequence 7, 105-10-106-106-106-106-106-106-106-106-106-	.6 352 6 US-10-888-962-8 Sequence 7,	.5 447 7 US-11-112-882-4 Sequence 4,	5 498 7 US-11-096-568A-5071 Sequence 507	5 500 7 US-11-096-568A-5070 Sequence 5070, 4 211 6 US-10-498-026-107	211 6 US-10-498-026-108 Sequence 108,	3 445 7 US-11-146-428-110 Sequence 110, 3 143 7 US-11-096-568A-6477 Sequence 6477,	3 175 7 US-11-096-568A-6476 Sequence 6476,	.9 181 / US-11-095-5684-6475 Sequence 6475, 3 461 6 US-10-467-65794 Sequence 6794, 3 211 6 US-10-498-026-109 Sequence 109,	
GenCore version 5 (c) 1993 - 2006 B	using sw	, 2006, 17:55:39 ; Search time 24 Seconds (without alignments) 12.997 Million cell updates/s	Title: US-10-772-537-4 Perfect score: 49 Sequence: 1 HSFSGVASVE 10	Gapext 0.	31191982	chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100%	Listing first 100 summaries	瓦	3: /SIDSS/ptodata/1/pubpaa/USO7 NEW PUB.pep: 4: /SIDSS/ptodata/1/pubpaa/PO7 NEW PUB.pep: 4: /SIDSS/ptodata/1/pubpaa/PO7 NEW PUB.pep: 4		••	umber of results predicted by chance to have a or equal to the score of the result heing wrinter	derived by analysis of the total score distribution.	SUMMARIES	DB ID Descripti	100.0 10 6 US-10-764-945-4 Sequence 4.	100.0 10 7 US-11-178-143-4 Sequence 4, 93.9 10 6 US-10-764-945-1 Sequence 1	93.9 10 6 US-10-764-945-5 Sequence 5,	93.9 10 b US-1U-764-945-6 Sequence 6, 93.9 10 7 US-11-178-143-1 Sequence 1,	93.9 10 7 US-11-178-143-5 Sequence 5, 93.9 10 7 US-11-178-143-6 Sequence 6	93.9 359 6 US-10-888-962-5 Sequence 5, 77.6 10 6 US-10-264-945-7	77.6 10 7 US-11-178-143-7 Sequence 7, 77.6 10 7 US-11-178-143-7 Sequence 7, 77.6 10 7 US-11-178-143-7	77.6 352 6 US-10-888-962-8 Sequence 7,	73.5 447 7 US-11-112-882-4 Sequence 4,	73.5 498 7 US-11-096-568A-5071 Sequence 507	73.5 500 7 US-11-096-568A-5070 Sequence 5070, 69.4 211 6 US-10-498-026-107	69.4 211 6 US-10-498-026-108 Sequence 108,	67.3 445 7 US-11-146-428-110 Sequence 110, 65.3 143 7 US-11-096-568A-6477 Sequence 6477,	65.3 175 7 US-11-096-568A-6476 Sequence 6476,	/ US-11-U98-5584-6475 Sequence 6475, 6 US-10-467-657-6794 Sequence 6794, 6 US-10-498-026-109 Sequence 109,	

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Sequence 1, Application US/10764945
Publication No. US20050282738A1
GENERAL INFORMATION:
APPLICANT: Teai, David.
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Prepar:
TITLE OF INVENTION: Thereof.
FILE REFERENCE: 2-04-01-26
CURRENT APPLICATION NUMBER: US/10/764,945
CURRENT FILING DATE: 2004-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT (CADAINSM: Bovine) COGANICM: Bovine (CATION: 300..309) THER INFORMATION: Polypeptide fragment from treatment of fetuin from bovine sera (CATER INFORMATION: described in the specification.
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Sequence 5. Application US/10764945
Publication No. US20050282738A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: US/10/764,945
CURRENT FILING DATE: 2004-01-26
PRICH APPLICATION NUMBER: US/10/145,682
PRICH APPLICATION NUMBER: US/10/145,682
PRICH APPLICATION NUMBER: 09/902,208
PRICH APPLICATION NUMBER: 09/902,208
PRICH APPLICATION NUMBER: 09/914,136
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                        TYPE: PRT
CRGANISM: Pig
LOCATION: 300..309
COTHER INFRAMIION: Polypeptide fragment from fetuin.
US-11-178-143-4
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PRIOR APPLICATION NUMBER: US/10/145,682
PRIOR PILING DATE: 2002-08-23
PRIOR FILING DATE: 2002-08-23
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 1099-10-07
PRIOR APPLICATION NUMBER: 09/414,136
PRIOR APPLICATION NUMBER: 09/149,878
PRIOR PILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFWARE: Microsoft Word 2001.
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0;
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Best Local Similarity 90.0
Matches 9; Conservative
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   LENGTH: 10
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1. TILE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati
1. TILE OF INVENTION: Thereof.
1. TILE OF INVENTION: THE STATE TO THE S
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   Sequence 20066, A
Sequence 9525, Ap
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TITLE OF INVENTION:
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer any
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer any
TITLE OF INVENTION: Thereof.
FILE REPRENCE: 2004-01892
CURRENT APPLICATION NUMBER: US/11/172,537
CURRENT FILING DATE: 2005-07-08
PRIOR PILING DATE: 2004-02-05
PRIOR FILING DATE: 2004-02-05
PRIOR FILING DATE: 1999-10-07
PRIOR PRILING DATE: 1999-10-07
PRIOR PRILING DATE: 1999-10-07
PRIOR PRILING DATE: 1999-10-07
PRIOR PRILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/149,878
PRIOR PRILING DATE: 1999-10-07
PRIOR APLICATION NUMBER: 09/149,878
PRIOR PRILING DATE: 1999-12-18
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CRGANISM: Pig

LOCATION: 300..309

JOHER INFORMATION: Polypeptide fragment from fetuin.

US-10-764-945-4
   US-11-096-568A-20066
US-11-087-099-9525
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                                                                                                                                                                                                                                                                                                  Segmence 4, Application US/10764945
Publication No. US20050282738A1
                                                                                                                                                                                                                                                                                                                                 PUDLICATION NO. US20050282738A1
GENERAL INFORMATION:
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SOFTWARE: Microsoft Word 2001.
SEQ ID NO 4
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Matches 10; Conservative
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ORGANISM: Bovine

LOCATION: 300..309

OTHER INFORMATION: Polypeptide fragment from treatment of fetuin from bovine ser

CTHER INFORMATION: described in the specification.
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US-11-178-143-5

US-11-178-143-5

US-11-178-143-5

SEQUENCE S. Application US/11178143

Publication No. US20050277594A1

GENERAL INFORMATION:
TILL DOF INVENTION:
TILLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
TILLE OF INVENTION: Thereof.
TILLE OF INVENTION: Thereof.
FILLS REFERENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/11/178,143

PRIOR FILLING DATE: 2004-02-05

PRIOR APPLICATION NUMBER: 10/145,682

PRIOR PILLING DATE: 2001-07-09

PRIOR PILLING DATE: 2001-07-09

PRIOR FILLING DATE: 1999-10-07

PRIOR FILLING DATE: 1999-10-07

PRIOR PILLING DATE: 1999-10-07

PRIOR FILLING DATE: 1998-10-07

PRIOR FILL
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; ORGANISM: Sheep
; LOCATION: 300..309
; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-11-178-143-5
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                            CURRENT FILING DATE: 2005-07-08
FRICR APPLICATION NUMBER: US/10/772,537
FRICR APPLICATION NUMBER: US/10/772,537
FRICR APPLICATION NUMBER: 10/145,682
FRICR FILING DATE: 2004-02-05
FRICR FILING DATE: 2002-05-14
FRICR FILING DATE: 2001-07-09
FRICR FILING DATE: 1094-04
FRICR FILING DATE: 1999-10-07
FRICR FILING DATE: 1999-10-07
FRICR FILING DATE: 1998-09-08
FRICR FILING DATE: 1998-09-08
FRICR FILING DATE: 1998-09-08
FRICR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
FUNDANT: 10
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Best Local Similarity 90.0
Matches 9; Conservative
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Publication No. US2005282738A1

GENERAL INFORMATION:

APPLICANT: Teai, David.

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati

TITLE OF INVENTION: Thereof.

FILE REFERENCE: 2-04-1892.

CURRENT APPLICATION NUMBER: US/10/764,945

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: US/10/145,682

PRIOR FILING DATE: 2001-07-09

PRIOR FILING DATE: 2001-07-09

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-12-18

NUMBER: 08/993,432

PRIOR FILING DATE: 1997-12-18

NUMBER: 08/993,432

PRIOR FILING DATE: 1997-12-18

SOFTWARE: Microsoft Word 2001.

SEQ ID NO 6

TWENT: DATE: 1097-12-18

TWENT: DATE: 1097-12-18
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Publication No. US20050277594A1

GAPERAL INFORMATION:

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati
TITLE OF INVENTION: Thereof.

FILE REFERENCE: 2-04-1892
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90.0%; Pred. No. 0.004;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            ORGANISM: Sheep
LOCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from fetuin.
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LOCATION: 300..309

1 LOCATION: Bolypeptide fragment from fetuin.

US-10-764-945-6
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Pred. No. 0.004;
1; Mismatches
PRIOR FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/149,878
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 08/993,432
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 5:
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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US-11-178-143-1
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Sequence 7, Application US/10764945

Sequence 7, Application US/10764945

Publication No. US20050282738A1

GENERAL INFORMATION:

APPLICANT: Teai, David.

TITLE OF INVENTION: Thareof.

TITLE OF INVENTION THAREOF.

CURRENT APPLICATION NUMBER: US/10/764,945

CURRENT APPLICATION NUMBER: US/10/145,682

PRIOR FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR PILING DATE: 1099-10-07

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-10-07

PRIOR PILING DATE: 1990-10-07

PRIOR PILING DATE: 1990-10-07

PRIOR PILING DATE: 1990-10-07

PRIOR PILING DATE: 1990-10-07
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WS-11-178-143-7

Sequence 7, Application US/11178143

Publication W. US2005027594A1

GENERAL INFORMATION:

APPLICANT: Tsai, David.

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Prepair TITLE OF INVENTION: Thereof.

TITLE OF INVENTION: Thereof.

FILE REFERRACE: 2-04-1892

CURRENT APPLICATION NUMBER: US/11/178,143

PRIOR PILING DATE: 2004-0-05

PRIOR PLING DATE: 2004-0-05

PRIOR PLING DATE: 2004-0-05

PRIOR PLING DATE: 1999-10-07

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR PLING DATE: 1999-0-07

PRIOR PLING DATE: 1999-0-07

PRIOR PLING DATE: 1999-10-07

PRIOR PLING DATE: 1999-12-18

WUMBER OF SEQ ID NOS: 7

SSOFID NO 7

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Mouse
LOCATION: 300..309
CTHEN TYPE: PRT
CTHEN TYPE: POLYPEPTIGE fragment from fetuin.
US-10-764-945-7
                                                                                                                        313 HTFSGVASVE 322
                                               1 HSFSGVASVE 10
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                                                                                                                                                                  US-11/8-143-6

j Edquence 4, Application US/11178143

j Publication No. US20050277594A1

j Edblication No. US20050277594A1

j GENERAL INFORMATION:

j APPLICANT: TSai, David

j TILE OF INVENTION:

j PRIOR APPLICATION NUMBER: US/10/772,537

j PRIOR PILING DATE: 2001-07-09

j PRIOR FILING DATE: 2001-07-09

j PRIOR FILING DATE: 2001-07-09

j PRIOR FILING DATE: 1999-10-07

j PRIOR FILING DATE: 1997-12-18

j SEQ ID NO 6

j SEQ ID NO 6

j TAVEN: DATE: DATE

j DATE

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Sequence 5, Application US/10868962;
Publication No. US20050566531A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ray, Ranjit
APPLICANT: Ray, Rannit
APPLICANT: Basu, Arnab
TITLE OF INVENTION: Growth
TITLE OF INVENTION: Growth
TITLE OF INVENTION: 2004-07-09
TITLE REPRERENCE: SLU 03-013 PCT
CURRENT FILING DATE: 2004-07-09
PRIOR PRILICATION NUMBER: 06/487,126
PRIOR PILING DATE: 2003-07-12
NUMBER: OF SEQ ID NOS: 15
SEQ ID NO 5
LEMORTH: BASO
LEMORTH: SASO
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Pred. No. 0.17;
1; Mismatches 0; Indels
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ORGANISM: Rat
LOCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from fetuin.
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Best Local Similarity 90.0%;
Matches 9; Conservative
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                                                                                                                   RESULT 8
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Gaps

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1; Indels

DB 6; Length 352;

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Score 38; DB 6
Pred. No. 5.8;
1; Mismatches
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                                                77.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.5%;
                                            Query Match 77.6
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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306 HAFSPVASVE 315
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ORGANISM: Pavlova salina
                                                                                                                                                                      1 HSFSGVASVE 10
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ORGANISM: Glycine max
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US-11-096-568A-5071
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US-11-112-882-4
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Sequence 7, Application US/1088962

Publication No. US20050266531A1

GENERAL INFORMATION:

APPLICANT: Saint Louis University

APPLICANT: Ray, Ranjit

APPLICANT: Ray, Ranjat

APPLICANT: Ray, Ranjat

TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell

TITLE OF INVENTION: Growth

TITLE OF INVENTION: Growth

TITLE OF INVENTION: 2004-07-09

TITLE OF INVENTION: 2004-07-09

FILE REFERENCE: SLU 03-013 PCT

CURRENT APPLICATION NUMBER: US/10/888,962

CURRENT FILING DATE: 2004-07-09

PRIOR FILING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.2

SEQ ID NO

TYPE: PRIOR TITLE OF THE OF THE
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APPLICANT: Raint Louis University
APPLICANT: Ray, Ranjit
APPLICANT: Ray, Ranjit
APPLICANT: Ray, Ranjit
APPLICANT: Ray, Ratna
APPLICANT: Basu, Arnab
TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
TITLE OF INVENTION: Composition School COURENT APPLICATION NUMBER: 60/487,126
PRIOR FILING DATE: 2004-07-09
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 15
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Pred. No. 5.7;
1; Mismatches 1; Indels
; TYPE: PRT
; ORGANISM: Mouse
; LOCATION: 300..309
; OTHER INFENATION: Polypeptide fragment from fetuin.
US-11-178-143-7
                                                                                                                                                                                          77.6%; Score 38; DB 7; 80.0%; Pred. No. 0.14;
                                                                                                                                                                                                                                                       1; Mismatches
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Publication No. US20050266531A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.6%;
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; ORGANISM: Rattus norvegicus
US-10-888-962-8
                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.6
Best Local Similarity 80.0
Matches 8; Conservative
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1 HAFSPVASVE 10
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US-10-888-962-7
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LENGTH: 352
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Sequence 4, Application US/11112882
Publication No. US20050273885A1
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Research Organisation
TITLE OF INVENTION: Synthesis of Long-Chain Polyunsaturated Fatty Acids in Recomb
FILE REPRENUE: 503244
CURRENT APPLICATION NUMBER: US/11/112,882
CURRENT FILING DATE: 2005-04-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5072, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypepti;
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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i LOCATION: (1)...(441)
i COCATION: (2)...(441)
i OTHER INFORMATION: Ceres Seq. ID no. 14306860
US-11-096-S68A-5072
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; Publication No. US20060051847A1
; GENERAL INFORMATION;
; APPLICANT: GUNNARSSON, NINA KATARINA
APPLICANT: BUILSER, JOCHEN
; APPLICANT: NEILSER, JOCHEN
; TITLE OF INVENTION: PRODUCTION OF POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 671306-2001.1
; CURRENT APPLICATION NUMBER: uS/11/146,428
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 60/577,245
; RIOR APPLICATION NUMBER: 60/577,245
; NUMBER OF SEQ ID NOS: 220
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; Sequence 108, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INPORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS;
; FILE REFERENCE: N.87430 WO GGW;
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT PILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 108
; LENGTH: 211
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Pred. No. 20;
1; Mismatches 1; Indels
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Pred. No. 70;
1; Mismatches 2; Indels
                                                                                   Length 211;
                                                                            69.4%; Score 34; DB 6; 77.8%; Pred. No. 20;
                                                                                                                                             1; Mismatches
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US-11-096-568A-6477
; Sequence 6477, Application US/11096568A
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 66. رود
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37 AFSGVASTE 45
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                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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US-11-146-428-110
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                   US-10-498-026-107
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592P025
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 5070
LENGTH: 500
APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 5071
LENGTH: 498
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Publication No. US20060024334A1
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS;
FILE REFERENCE: N. 87430 WO GGW
CURRENT APPLICATION OF GGW
CURRENT PILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 118
SOF ID NO 107
LENGTH: 211
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Pred. No. 21;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 7;
Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1). _ (498)
; OTHER INFORMATION: Ceres Seq. ID no. 14306859
US-11-096-568A-5071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LCCATION: (1)..(500)
; OTHER INFORMATION: Ceres Seq. ID no. 14306858
US-11-096-568A-5070
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ORGANISM: Euroglyphus maynei
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Best Local Similarity 70.v
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVERTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
FILE REPERENCE:
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NO 6794
SEQ ID NO 6794
LENGTH: 461
                                                                                                                                                                      Length 181;
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                                                                                                                                                                                                              1; Indels
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Publication No. US20060024334A1
GENERAL INFORMATION:
APPLICANT CIVENTION:
IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
FILE REFERENCE: N. 87430 WO GCW
CURRENT APPLICATION NUMBER: US/10/498,026
CURRENT APPLICATION NUMBER: 2044-06-04
NUMBER OF SEQ ID NOS: 118
SOPTWARE: Patentin version 3.1
                                                                                                                                                                  Score 32; DB 7;
Pred. No. 43;
1; Mismatches
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Pred. No. 78;
                                             2; Mismatches
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6794
                                                                                                                                                                65.3%;
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Best Local Similarity 66.7%;
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; ORGANISM: Euroglyphus maynei
US-10-498-026-109
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Best Local Similarity 66.
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Matches 7; Conservative
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91 HSFVGLAAV 99
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        TYPE: PRT
ORGANISM: Glycine max
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LENGTH: 211
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                                 APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PW32
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
ENOTH: 143
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Publication No. US20060048240A1
GENERAL INFORMATION:
FURTLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6476
LENGTH: 175
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 105-1592PUSC
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6475
LENGTH: 181
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                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 7;
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(143)
OTHER INFORMATION: Ceres Seq. ID no. 14315300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1).: (175)
; OTHER INFORMATION: Ceres Seq. ID no. 14315299
US-11-096-568A-6476
Publication No. US20060048240A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   65.3%;
                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
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US-11-096-568A-6476
                                                                                                                                                                                                                                                                                                                                         US-11-096-568A-6477
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APPLICATION TO A COLORDIA

TITLE OF INVENTION: Coronavirus, nucleic acid, protein, and methods for the general INVENTION: Variable of the medicaments and diagnostics.

TITLE OF INVENTION: vaccine, medicaments and diagnostics.

FILE REFERENCE: 294-226

CURRENT APPLICATION NUMBER: US/10/922,232B

CURRENT FILING DATE: 2004-08-18

PRIOR FILING DATE: 2004-01-07

PRIOR FILING DATE: 2004-01-07

PRIOR FILING DATE: 2003-08-18

PRIOR FILING DATE: 2004-01-07

NUMBER: EP 04075050.7

NUMBER: EP 04075050.7

NUMBER: Patentin version 3.1

SEQ ID NO 65
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                    APPLICANT: Chua, Kaw-yan
TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS OF
TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS OF
TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITE)
FILE REFERENCE: IMI-005CNDV2
CURRENT APPLICATION NUMBER: US/10/746,909
CURRENT FILING DATE: 2003-12-29
FRIOR FILING DATE: 1993-12-29
FRIOR PILING DATE: 1993-08-16
FRIOR PILING DATE: 1993-08-16
FRIOR FILING DATE: 1990-09-11
FRIOR FILING DATE: 1990-09-11
FRIOR FILING DATE: 1990-02-13
FRIOR FILING DATE: 1990-02-13
FRIOR FILING DATE: 1990-02-13
FRIOR FILING DATE: 1990-03-11
FRIOR FILING DATE: 1990-03-13
FRIOR
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; Sequence 11161, Application US/11087099
; Publication No. US20060041961A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/10922232B Publication No. US20060024668A1 GENERAL INFORMATION:
      APPLICANT: Wayne, Robert Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Dermatophagoides sp
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ORGANISM: Artificial Sequence
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Matches 6; Conservative
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37 AFSGVAATE 45
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; Sequence 2, Application US/10746909
; Publication No. US20060008973A1
; GENERAL INFORMATION:
    APPLICANT: Hayne, Robert Thomas
; APPLICANT: Hayne, Robert Thomas
; APPLICANT: Hayne, Robert Thomas
; TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS OF
    TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITE)
; TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITE)
; FILE REFERENCE: IM-005CNBV2
; CURRENT APPLICATION NUMBER: 0310-12-3
; PRIOR FILING DATE: 1993-12-29
; PRIOR FILING DATE: 1993-08-16
; PRIOR FILING DATE: 1993-09-11
; PRIOR PRILING DATE: 1990-09-11
; PRIOR PRILING DATE: 1990-02-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 2
; LENGTH: 222
                                                                                                                                                                               Sequence 110, Application US/10498026

Publication No. US20060024334A1

GENERAL INPORMATION:

APPLICANT: CIRCASIA LIMITED

TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS

FILE REFERENCE: N.87430 WO GCW

CURRENT APPLICATION NUMBER: US/10/498,026

CURRENT FILING DATE: 2004-06-04

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.1

SEQ ID NO 110

LENGTH: 212
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Pred. No. 79;
2; Mismatches 1; Indels
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ORGANISM: Buroglyphus maynei
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
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37 AFSGVAATE 45
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38 AFSGVAATE 46
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APPLICANT: Crameri, Reconstructions and process of the constructs of the construction of the construction of the constructs of the construction of the c
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| Publication No. US20060003414A1
| GENERAL INFORMATION:
| APPLICANT Mateui, Tomoko
| APPLICANT: Draborg, Henriette
| APPLICANT: Danielsen, Steffen
| TITLE OF INVENTION: Signal Peptide for Producing a Polypeptide
| TITLE OF INVENTION: Signal Peptide for Producing a Polypeptide
| CURRENT APPLICATION NUMBER: US/11/152,811
| CURRENT FILING DATE: 2005-06-14
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: Patentin Version 3.3
| SEQ ID NO 3.3
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                    ; Sequence 20, Application US/11102883
; Publication No. US20050281816A1
; GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                             APPLICANT: Lamping, Norbert APPLICANT: Crameri, Reto
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                134 AFSGVAATE 142
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LOCATION: (99)..(320)
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Best Local Similarity
Matches 6; Conserva
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LOCATION: (19)...(98)
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LOCATION: (1)..(18)
                                                                                                                                      JS-11-102-883-20
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TYPE: PRT
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Publication No. US20060024334A1
GENERAL INFORMATION:
APPLICANT: CIRCASIA LIMITED
TILE OF INVENITON: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
FILE REFERENCE: N.87430 WO GCW
CURRENT APPLICATION NUMBER: US/10/498,026
CURRENT FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 118
SQTWARE: Patentin version 3.1
SQTWARE: Patentin version 3.1
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                              Length 307;
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66.7%; Pred. No. 1.2e+02;
tive 1; Mismatches 2; Indels
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Publication No. US20060024334A1
GENERAL INPORMATION:
TILE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
FILE REFERENCE: N.87430 WO GCW
CURRENT APPLICATION NUMBER: US/10/498,026
CURRENT FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 118
                       APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EF
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11161
                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Trichodesmium erythraeum IMS101
US-11-087-099-11161
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ORGANISM: Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Dermatophagoides farinae US-10-498-026-21
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Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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133 AFSGVAATE 141
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GENERAL INFORMATION:
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US-10-498-026-21
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LENGTH: 320
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US-10-63-155-170
Sequence 170, Application US/10623155
Publication No. US20050261166A1
SEQUENCE INFORMATION:
APPLICANT: Ward W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT PILING DATE: 2003-07-17
CURRENT FILING DATE: 2003-07-17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 170
LENGTH: 791
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| Sequence 430, Application US/10623155
| Sequence 430, Application US/2050261166A1
| Sequence 430, Application No. US20050261166A1
| GENERAL INFORMATION:
| APPLICANT: Wang, Tongtong
| APPLICANT: Retter, David W. | APPLICANT: Retter, Marc W. | APPLICANT: Retter, Gary R. | TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITION: OWN DOSITIONS OF LUNG CANCER | FILE REFERENCE: 210121.455C20 | CURRENT APPLICATION NUMBER: US/10/623,155 | CURRENT APPLICATION NUMBER: 2003-07-17 | NUMBER OF SEQ ID NOS: 560 | NUMBER OF SEQ ID NOS: 560 | SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Retter, Marc W.
APPLICANT: Frager, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT PILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 592
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Pred, No. 2.3e+02;
3; Mismatches 2; Indels
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Best Local Similarity 50.0%;
Matches 5; Conservative
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346 HTFVGIASFD 355
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346 HTFVGIASFD 355
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ORGANISM: Homo sapiens
US-10-623-155-169
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US-10-623-155-170
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                                                         RESULT 35

US-11-102-883-28

i Sequence 28, Application US/11102883

s Sequence 28, Application US/11102883

s Publication No. US20050281816A1

GENERAL INFORMATION:
APPLICANT: Lamping, Norbert
APPLICANT: Crameri, Reto
APPLICANT: Crameri, Reto
APPLICANT: Grameri, Reto
APPLICANT: Grameri, Reto
APPLICANT: Grameri, Reto
APPLICANT: Grameri, Reto
APPLICANT: Gradiar Instance
TITLE OF INVENTION: Wodular Antigen Transporter Molecules (MAT Molecules) for
TITLE OF INVENTION: Wodular Antigen Transporter
FILIS REFERENCE: 03100234pa
CURRENT APPLICATION NUMBER: US/11/102,883

CURRENT FILING DATE: 2002-10-11

PRIOR FILING DATE: 2002-10-11

PRIOR FILING DATE: 2003-10-11

PRIOR FILING DATE: 2003-10-11

PRIOR FILING DATE: 2003-10-11

SRIOR FILING DATE: 2003-10-11

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.2

LENGTH. 21
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Publication No. US20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 5245
LENGTH: 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ; ORGANISM: Schizosaccharomyces pombe US-11-087-099-5245
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Best Local Similarity 66./-
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Matches 6; Conservative
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) ORGANISM: tat-Ii-der p 1
US-11-102-883-28
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     165 AFSGVAATE 173
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US-11-087-099-5245
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Sequence 10150, Application US/11098686

Publication No. US22066024696A1

GENERAL INFORMATION:

APPLICANT: KADUX, Viek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REFERENCE: 09531-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT PILING DATE: 2005-04-04

PRIOR PILING DATE: 2003-10-01

PRIOR PILING DATE: 2003-10-04

NUMBER: OF SEQ ID NOS: 11433

SOFTWARE: FBSEC for Windows Version 4.0

SEQ ID NO 10150

LENGTH: 1089
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Sequence 3838, Application US/10467657

Publication Wo. US200S0260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: PIZZA Maria Rita

APPLICANT: PIZZA Maria Rita

APPLICANT: MASIGNANI Vega

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REPERENCE:

CURRENT APPLICATION NUMBER: 203-08-11

PRIOR APPLICATION NUMBER: 203-08-11

PRIOR APPLICATION NUMBER: 203-08-11

PRIOR PILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SEQ ID NO 3838

SEQ ID NO 3838
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Pred. No. 70;
0; Mismatches 2; Indels
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Pred. No. 4.4e+02;
1; Mismatches 1;
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; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Lawsonia intracellularis
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Best Local Similarity 75.0
Matches 6; Conservative
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Matches 7; Conservative
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                                                                                                US-11-098-686-10150
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US-10-467-657-9192
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; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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; TITLE OF TITLE OF LUNG CANCER
; TITLE OF
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; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongeng
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 161
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. 3.5e+02;
2; Indels
                                                                                                                           Length 881;
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                                                                                                                  Score 31; DB
Pred. No. 3.5e
3; Mismatches
                                                                                                                  63.3%;
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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346 HTFVGIASFD 355
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-430
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    RESULT 40
US-10-623-155-357
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                                                                                                                                                                                                                                                                                      Query Match 61.2%; Score 30; DB 6; Length 330; Best Local Similarity 40.0%; Pred. No. 2e+02; Matches 4; Conservative 5; Mismatches 1; Indels
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85.7%; Pred. No. 2.3e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 976, Application US/11087099
Publication No. US20060041961A1
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION UNHBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 387
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Publication No. US20060041961A1
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERENCE: 38-21(53450) B EP
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Gaeumannomyces graminis var. tritici
US-11-087-099-976
PRIOR APPLICATION NUMBER: JP 10-292348
PRIOR FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 10
LENGTH: 330
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                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-887-475B-10
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Best Local Similarity 85.7
Matches 6; Conservative
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285 SGVASIE 291
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US-11-087-099-6374
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US-11-087-099-8098
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LENGTH: 387
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Publication No. US20060005201A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Agricultural Science

TITLE OF INVENTION: A production of plants having improved rooting efficiency and vae

TITLE OF INVENTION: A production of plants sessistant gene

TITLE OF INVENTION: Using environmental stress-resistant gene

CURRENT APPLICATION NUMBER: US/10/798,579A

CURRENT APPLICATION NUMBER: US/10/798,579A

CURRENT FILING DATE: 2004-03-12

PRIOR FILING DATE: 2003-03-14

NUMBER OF SEQ ID NOS: 30

LENGTH 2330
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                      APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Eliabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 9192
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| Publication No. US20060015973A1
| GENERAL INFORMATION:
| APPLICANT: SHIGHAL
| APPLICANT: SAKUMA, Yoh
| TITLE OF INVENTION: Environmental stress-tolerant plants
| TITLE OF INVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 6; Length 330;
Pred. No. 2e+02;
5; Mismatches 1; Indels
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66.7%; Pred. No. 1.1e+02;
ive 1; Mismatches 2; Indels
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ORGANISM: Neisseria gonorrhoeae
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ORGANISM: Arabidopsis thaliana
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APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
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Matches 6; Conservative
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23 HTFSGEAPV 31
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61.2%; Score 30; DB 7; Length 387;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abad, wark S. et al.
TITLE OF INVENTION:
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 8098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9490, Application US/11087099
PUblication No. US20060041961A1
GENERAL INFORMATION: US20060041961A1
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ; ORGANISM: Gaeumannomyces graminis var. tritici US-11-087-099-9490
                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Gaeumannomyces graminis var. avenae US-11-087-099-8098
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Job time : 25 secs
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285 SGVASIE 291
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285 SGVASIE 291
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Sequence 4, Application US/10772537
Publication No. US20040259800A1
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Prepar TITLE OF INVENTION: Thereof.
FILE REFERENCE: 2-04-1892
CURRENT APPLICATION NUMBER: US/10/772,537
CURRENT FILING DATE: 2004-02-05
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsai, David.
TITLE OF INVENTION: Polyspetide for the Treatment of Cancer and a Method
TITLE OF INVENTION: of Preparation
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
CURRENT APPLICATION NUMBER: US/10/267,706
CURRENT APPLICATION NUMBER: US/10/267,706
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  100.0%; Score 49; DB 4; Length 10; 100.0%; Pred. No. 0.0027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 300..309
; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-267-706-4
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PRIOR APPLICATION NUMBER: US/10/145,682A
PRIOR FILING DATE: 2002-08-23
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/414,136
PRIOR APPLICATION NUMBER: 09/149,878
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: 08/993,432
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PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/414,136
PRIOR APPLICATION NUMBER: 09/419, 136
PRIOR APPLICATION WUMBER: 09/149, 878
PRIOR FILING DATE: 1998-09-08
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PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10267706
Publication No. US20030087809A1
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
SEQ ID NO 4
LENGTH: 10
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Best Local Similarity 100.0
Matches 10; Conservative
Query Match
Best Local Similarity 100.
Matches 10; Conservative
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TITLE OF INVENTION: Thereof.

FILE REPRENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/221,662

CURRENT FILING DATE: 2002-09-16

PRIOR FILING DATE: 2001-07-09

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 7

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Squence 4, Application US/10145682A

Publication No. US2030027767A1

GENERAL INFORMATION:

APPLICATION To avid.

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Mer

TITLE OF INVENTION: Thereof.

FILE REFERENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/145,682A

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR APPLICATION NUMBER: 09/149,878

PRIOR PILING DATE: 1999-10-07

PRIOR APPLICATION NUMBER: 08/993,432

PRIOR PLING DATE: 1999-12-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Microsoft Word 2001.
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100.0%; Score 49; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT (CRANISM: Pig 100-1010); TYPE: PRT (CRANISM: Pig 100-1010); DOTHER INFORMATION: Polypeptide fragment from fetuin. US-10-145-682A-4
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, OTHER INFORMATION: Polypeptide fragment from fetuin. US-10-221-662-4
                                                    ALIGNMENTS
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Publication No. US20030050446Al
GENERAL INFORMATION:
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ORGANISM: Pig
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Sequence 6, Application US/10145682A
| Publication No. US20030027767A1
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Tsai, David |
| TITLE OF INVENTION: Thereof. |
| TITLE OF INVENTION: Thereof. |
| FILE REPERANCE: 2-04-1892 |
| CURRENT APPLICATION NUMBER: US/10/145,682A |
| CURRENT FILING DATE: 2002-08-23 |
| PRIOR APPLICATION NUMBER: 09/902,208 |
| PRIOR PILING DATE: 1999-10-07 |
| PRIOR FILING DATE: 1999-10-07 |
| PRIOR FILING DATE: 1999-0-08 |
| PRIOR FILING DATE: 1999-0-08 |
| PRIOR FILING DATE: 1999-0-08 |
| PRIOR FILING DATE: 1997-12-18 |
| NUMBER OF SEQ ID NOS: 7 |
| SOFTWARE: MICROSOFT WORD |
| SOFTWARE: MICROSOFT WORD |
| CONTRACT |
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Publication No. US20030050446A1
GENERAL INFORMATION:
PAPLICANT: Tsai, David.
TITLE OF INVENTION: Thereof.
FILE OF INVENTION: Thereof.
FILE REFERENCE: 2-04-1892
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 09/902,208
PRIOR PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/414,136
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; ORGANISM: Sheep
; LOCATION: 300..309
; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-145-682A-5
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; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-145-682A-6
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90.0%; Pred. No. 0.011;
tive 1; Mismatches
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Pred. No. 0.011;
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          PRIOR APPLICATION NUMBER: 08/993,432
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFFWARE: Microsoft Word 2001.
LENGTH: 10
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Rat
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US-10-221-662-1
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TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati;
TITLE OF INVENTION: Thereof.

FILE REPERENCE: 2-04-189.

CURRENT APPLICATION NUMBER: US/10/145,682A

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR FILING DATE: 1999-10-07

PRIOR PILING DATE: 1999-10-07

PRIOR PILING DATE: 1998-10-07

PRIOR PILING DATE: 1998-09-08

PRIOR FILING DATE: 1999-10-07

PRIOR PILING DATE: 1999-10-07

PRIOR PILING DATE: 1999-06

PRIOR PILING DATE: 1991-12-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Microsoft Word 2001.
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Publication No US20030027767A1
GENERAL INFORMATION:
GENERAL TEAM, DAVId.
TITLE OF INVENTION: POlypeptide for the Treatment of Cancer and a Method of Preparation Title OF INVENTION: Thereof.
FILE REFERENCE: 2-04-1892.
CURRENT APPLICATION NUMBER: US/10/145,682A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/414,136
PRIOR FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT:
ORGANISM: Bovine
COCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from treatment of fetuin from bovine sera as OTHER INFORMATION: described in the specification.
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                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                 Query Match 100.0%; Score 49; DB 5; Length 10 Best Local Similarity 100.0%; Pred. No. 0.0027; Matches 10; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
93.9%; Score 46; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels
                                                     TYPE: PRT

CRGANISM: Pig

LOCATION: 300..309

THER INCRATION: Polypeptide fragment from fetuin.
US-10-772-537-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10145682A Publication No. US20030027767A1 GENERAL INFORMATION:
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SEQ ID NO 4
LENGTH: 10
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Sequence 1, Application US/10267706;
Publication No. US20030087809A1
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method
TITLE OF INVENTION: Of Preparation
TITLE OF INVENTION: Of Preparation
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Of Preparation
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: UNMER: US/10/267,706
CURRENT APPLICATION NUMBER: US/10/45,682A
CURRENT FILING DATE: 2002-10-08
PRIOR FILING DATE: 2001-09-09
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-00-08
PRIOR FILING DATE: 1999-00-08
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-00-08
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
LENGTH: 10
THE NOS: 7
TENGTH: 10
THE NOS: 7
TENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.9%; Score 46; DB 4; Length 10; 90.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from fetuin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bovine
LOCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from treat
OTHER INFORMATION: bovine sera as
OTHER INFORMATION: described in the specification.
US-10-267-706-1
                            CURRENT APPLICATION NUMBER: US/10/221,662
CURRENT FILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-16
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 1999-10-07
PRIOR PILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-0-08
PRIOR FILING DATE: 1999-0-08
PRIOR FILING DATE: 1999-0-08
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 7
SCOTTAME: Microsoft Word 2001.
SEQ ID NO 6
LENGTH: 10
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Matches 9, Conservative
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Best Local Similarity
Matches 9; Conserv
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ORGANISM: Rat
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US-10-267-706-1
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| Publication No. US20030050446A1
| GENERAL INFORMATION:
| APPLICANT: Tsai, David.
| TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati
| TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and Method of Preparati
| TITLE OF INVENTION: Thereof.
| FILE REFERENCE: 2-04-1892
| CURRENT APPLICATION NUMBER: US/10/221,662
| CURRENT PILING DATE: 2002-09-16
| PRIOR FILING DATE: 1999-10-07
| PRIOR FILING DATE: 1999-10-07
| PRIOR APPLICATION NUMBER: 09/149,878
| PRIOR APPLICATION NUMBER: 09/149,878
| PRIOR APPLICATION NUMBER: 09/0-08
| PRIOR APPLICATION NUMBER: 09/9-08
| PRIOR APPLICATION NUMBER: 09/9-08
| PRIOR PILING DATE: 1999-10-07
| PRIOR APPLICATION NUMBER: 09/9-08
| PRIOR PILING DATE: 1997-12-18

    i LOCATION: 300..309
    OTHER INFORMATION: Polypeptide fragment from treatment of fetuin from bovine sera as
    i OTHER INFORMATION: described in the specification.
    US-10-221-662-1

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TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati
TITLE OF INVENTION: Thereof.
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; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-221-662-5
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PRIOR FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: 09/149,878
PRIOR PILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 08/993,432
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
SEQ ID NO 1
LENGTH: 10
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Publication No. US20030050446A1
GENERAL INFORMATION:
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SOFTWARE: Microsoft Word 2001.
SEQ ID NO 5
LENGTH: 10
TYPE: PRT
ORGANISM: Sheep
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Matches 9; Conservative
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1 HTFSGVASVE 10
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US-10-221-662-6
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                                                                                            GENERAL INFORMATION:

FOR INTERIOR INFORMATION:

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method

TITLE OF INVENTION: Of Preparation

TITLE OF INVENTION: Thereof.

FILE REPERBACE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/145,682A

PRIOR FILING DATE: 2002-08-23

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 1999-10-07

SEOUTHARE: Microsoft Word 2001.
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Publication No. US20030087809A1

GENERAL INPORMATION:

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method

TITLE OF INVENTION: Of Preparation

TITLE OF INVENTION: Of Preparation

TITLE OF INVENTION: Thereof.

TITLE OF INVENTION: Thereof.

FILE REFERENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/267,706

CURRENT APPLICATION NUMBER: US/10/145,682A

FRIOR APPLICATION NUMBER: 09/902,208

FRIOR FILING DATE: 2001-07-09

FRIOR FILING DATE: 1999-10-07

FRIOR FILING DATE: 1999-10-07

FRIOR FILING DATE: 1999-10-07

FRIOR APPLICATION NUMBER: 09/144,136

FRIOR FILING DATE: 1999-10-07

FRIOR FILING DATE: 1998-00-08

FRIOR FILING DATE: 1998-01-08

FRIOR FILING DATE: 1998-01-08

FRIOR FILING DATE: 1998-01-08

FRIOR FILING DATE: 1998-01-08

FRIOR APPLICATION NUMBER: 08/149,432

FRIOR FILING DATE: 1998-01-08

FRIOR FILING DATE: 1998-01-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Sheep
LOCATION: 300..309
CHER INFRANTION: Polypeptide fragment from fetuin.
US-10-267-706-5
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; ORGANISM: Rat
; LOCATION: 300..309
; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-267-706-6
Sequence 5, Application US/10267706 Publication No. US20030087809A1 GENERAL INFORMATION:
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Best Local Similarity 90.0
Matches 9; Conservative
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HTFSGVASVE 10
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Sequence 1. Application US/10772537;
Publication No. US20040259800A1
GENERAL INFORMATION:
JENDICAMIN: TBai, David.
TITLE OF INVENTION: Thereof.
FILE REFERENCE: 2-04-1892.
CURRENT APPLICATION NUMBER: US/10/772,537
CURRENT PILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: 09/02,208
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 1999-10-07
PRIOR PILING DATE: 1999-10-07
PRIOR PRIOR PILING DATE: 1999-10-07
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Sequence 5, Application US/10772537
Sequence 5, Application WS/10772537
Sequence 5, Application No. US2004025980A1
SENDICATION NO. US2004025980A1
STILE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
STILE OF INVENTION NUMBER: 10/145,682
SPICH APPLICATION NUMBER: 09/914,136
SPICH PLING DATE: 2001-07-09
SPICH PLING DATE: 1999-10-07
SPICH FILING DATE: 1999-10-07
SPICH STILING DATE: 1999-10-07
SPICH SPILING DATE: 1997-12-18
SPICH SPILING DATE: 1997-12-18
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CRGANISM: Bovine
COCATION: 3100..309
OTHER INFORMATION: Polypeptide fragment from treatment of fetuin from bovine ser
COTHER INFORMATION: described in the specification.
US-10-772-537-1
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          Score 46; DB 4; Length 10;
Pred. No. 0.011;
1; Mismatches 0; Indels
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Pred. No. 0.011;
1; Mismatches
       93.9%;
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Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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Sequence 7, Application US/10145682A;
Sequence 7, Application US/10145682A;
Sequence 7, Application US/20030027767A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Tati. David.
TITLE OF INVENTION: Playeptide for the Treatment of Cancer and a Method of Prepar TITLE OF INVENTION: Playeptide for the Treatment of Cancer and a Method of Prepar TITLE OF INVENTION: UNMERS: US/10/145,682A;
TITLE REPERENCE: 2-04-1892
CURRENT PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/902,208
PRIOR APPLICATION NUMBER: 09/414,136
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-12-18
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
SEQ ID NO 7
LENGTH: 10
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Publication No. US20030050446A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Prepar TITLE OF INVENTION: Thereof.
TITLE REFERENCE: 2-04-1892
CURRENT APPLICATION NUMBER: US/10/221,662
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-09
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0.62;
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                                                                                                                                                                                                                                                                                         Score 46; DB Pred. No. 0.621; Mismatches
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PRIOR APPLICATION NUMBER: PCT/USO1/42832
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/243,442
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 7
SOFWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 359
                                                                                                                                                                                                                                                                                         93.9%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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313 HTFSGVASVE 322
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                                                                                                                                                                                             TYPE: PRT
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Sequence 6, Application US/10772537

Publication No. US20040259800A1

GENERAL INFORMATION:

APPLICANT: Tasi, David.

TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati

TITLE OF INVENTION: Thereof.

FILE REFERENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/772,537

CURRENT APPLICATION NUMBER: US/202-05-14

PRIOR APPLICATION NUMBER: 09/902,208

PRIOR FILING DATE: 2001-07-09

PRIOR FILING DATE: 1999-10-07

PRIOR APPLICATION NUMBER: 09/414,136

PRIOR PLING DATE: 1999-00-08

PRIOR PLING DATE: 1999-10-07

PRIOR APPLICATION NUMBER: 09/414,436

PRIOR PLING DATE: 1999-10-07

PRIOR PLING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 7

SEQ ID NOS: 7

SEQ ID NOS: 7

LENGTH 10
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Publication No. US20040198648A1
GENERAL INFORMATION:
APPLICANT: GRUNBERGER, George
APPLICANT: GRUNBERGER, Catherine Jen
APPLICANT: KAI-LIN, Catherine Jen
APPLICANT: SINIVAS, Pochur, R.
TITLE OF INVENTION: IN OBESITY AND INSULIN CONTROL OF GLUCOSE HOMEOSTASIS
FILE REFERENCE: 38168-18776
; CURRENT APPLICANION NUMBER: US/10/415,288
; CURRENT FILING DATE: 2003-04-28
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pred. No. 0.011;
1; Mismatches 0; Indels
                                                                                                                                                                                                                   93.9%; Score 46; DB 5; Length 10; 90.0%; Pred. No. 0.011; tive 1; Mismatches 0; Indels
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ORGANISM: Rat
LOCATION: 300..309
CTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-772-537-6
                                                                             ; TYPE: PRT
; ORGANISM: Sheep
; LOCATION: 300..309
; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-772-537-5
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         SOFTWARE: Microsoft Word 2001.
SEQ ID NO 5
LENGTH: 10
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Matches 9; Conservative
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1 HTFSGVASVE 10
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1 HTFSGVASVE 10
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Best Local Similarity
Matches 9; Conserva
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Sequence 5, Application US/10415288
Publication No. US20040198648A1
GENERAL INPORMATION:
APPLICANT: GENERAL GEORGE
APPLICANT: MATTHEWS, Suresh T.
APPLICANT: MATTHEWS, Suresh T.
APPLICANT: MATTHEWS, Sorterine Jen
APPLICANT: SRINIVAS, Pothur, R.
TITLE OF INVENTION: INHIBITION OF ALPHA-2 HS GLYCOPROTEIN (AHSG/FETUIN)
TITLE OF INVENTION: IN OBESITY AND INSULIN CONTROL OF GLUCOSE HOMEOSTASIS
FILE REPERENCE: 38368-187769
CURRENT PILING DATE: 2003-04-28
CURRENT PILING DATE: 2003-04-28
FRIOR APPLICATION NUMBER: US 60/243,442
PRIOR PELLING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 7
SEQ ID NO S
LENGTH: 346
LENGTH: 346
LENGTH: 346
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; LOCATION: 300..309
; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-772-537-7

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80.0%; Pred. No. 0.52;
                                TILE REPERBNCE: 2-04-1892
CURRENT APPLICATION NUMBER: US/10/772,537
CURRENT FILIDE DATE: 2004-02-05
RIDE REPERBNCE: 2004-02-05
PRIOR APPLICATION NUMBER: 10/145,682
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR PILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
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                             Thereof.
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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Publication No. US20040259800A1
GENERAL INFORMATION:
APPLICANT: Tsal, David.
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati
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Publication No. US20030087809A1

GENERAL INPORMATION:
I TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method
ITITLE OF INVENTION: of Preparation
CURRENT APPLICATION NUMBER: US/10/267,706

CURRENT APPLICATION NUMBER: US/10/145,682A

PRIOR PRIOR APPLICATION NUMBER: 09/902,208

PRIOR FILING DATE: 2001-07-08

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 1998-10-09

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 1998-10-08

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                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from fetuin.
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; ORGANISM: Mouse
; LOCATION: 300..309
; OTHER LINERALION: Polypeptide fragment from fetuin.
US-10-267-706-7
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PRIOR FILING DATE: 1999-10-07
PRIOR PEDLICATION NUMBER: 09/149,878
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 08/99,432
PRIOR PILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: MICROSOFT WORD OF SEQ ID NOS: 7
SEQ ID NO 7
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1 HAFSPVASVE 10
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                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mouse
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TITLE OF INVENTION: IN OBESITY AND INSULIN CONTROL OF GLUCOSE HOMEOSTASIS FILE REFERENCE: 38368-187769
CURRENT APPLICATION NUMBER: US/10/415,288
CURRENT PILING DATE: 2003-04-28
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                 77.6%; Score 38; DB 4; Length 352; 80.0%; Pred. No. 28; ive 1; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
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CURRENT PAPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
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Patent No. US20020132240A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Williams, P. Mickey
Wood, William, I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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US-10-415-288-6
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, David
APPLICANT: Eaton, Dan L.
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Best Local Similarity 80.0
Matches 8; Conservative
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Gao, Wei-Qiang
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APPLICANT: MATTHEWS, Suresh T.
APPLICANT: KAI-LIN, Catherine Jen
APPLICANT: GOUSTIN, Anton, Scott
APPLICANT: SRINIVAS, POTHNY, R.
TITLE OF INVENTION: INHIBITION OF ALPHA-2 HS GLYCOPROTEIN (AHSG/FETUIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 28;
1; Mismatches 1; Indels
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APPLICANT: Peters, Kevin
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT APPLICATION NUMBER: US 60/355,295
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR APPLICATION NUMBER: US 60/355,295
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 86
LENGTH: 352
                                                                                          APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT PILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR APPLICATION NUMBER: US 60/355,295
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PATENTI VERSION 3.1
SEQ ID NO 84
LENGTH: 352
TYPE: PRT
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Pred. No. 28;
                                  : The Procter & Gamble Company
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; Publication No. US20040198648A1
; GENERAL INFORMATION:
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Rattus norvegicus US-10-316-253-84
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ORGANISM: Rattus norvegicus
                                                                         Thompson, Larry
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                       Peters, Kevin
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306 HAPSPVASVE 315
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Best Local Similarity
8; Conserv?
           GENERAL INFORMATION
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                                                     APPLICANT:
APPLICANT:
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Length 713;
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Pred. No. 1e+02;
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
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Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Achkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P
Pan, James
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Best Local Similarity 60.0
Matches 6; Conservative
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Sao, Wei-Qiang
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|135 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-245
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1e+02;
4; Mismatches 0; Indels
                                          FRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR PRIOR PRIOR DATE: 1999-11-29
PRIOR PRIOR DATE: 1999-11-29
PRIOR PRIOR DATE: 1999-11-29
PRIOR PRIOR DATE: 1999-11-20
PRIOR PRIOR DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-04
PRIOR PRIOR DATE: 1999-12-20
PRIOR PRIOR DATE: 1999-12-30
PRIOR PRIOR DATE: 1999-12-30
PRIOR PRIOR DATE: 1999-12-30
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PRIOR PRIOR PRIOR DATE: 3090-12-30
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                                PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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Patent No. US20020146709A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Hillan, Kenneth, J.
      1999-09-15
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Goddard, A.
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Mather, Jennie P.
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Gao, Wei-Qiang
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135 HSFAGLASLQ 144
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; ORGANISM: Homo Sapien
US-09-909-320-245
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION UNMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
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PRIOR PELICATION NUMBER: US/09/665,350
PRIOR PELING DATE: 1090-07-18
PRIOR PELING DATE: 1090-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
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PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PRIOR DATE: 1999-12-07
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
                                     Gerber, Hanspeter
Gerritsen, Mary E
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Paoni, Nicholas F.
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      Wei-Qiang
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|135 HSFAGLASLQ 144
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                    PAPLICANTIN NOOM, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic FILE REFERENCE: 10466-112

CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FLING DATE: 2001-07-12

FRIOR PILING DATE: 2000-07-12

FRIOR PAPLICATION NUMBER: US 60/145,698

FRIOR APPLICATION NUMBER: US 60/146,222

FRIOR APPLICATION NUMBER: US 60/146,222

FRIOR PILING DATE: 1999-07-07-8

FRIOR PILING DATE: 1999-07-08

FRIOR PILING DATE: 1999-07-08

FRIOR PILING DATE: 1999-07-08

FRIOR PILING DATE: 1999-07-18

FRIOR PILING DATE: 1999-09-08-08

FRIOR PILING DATE: 1999-09-08-08

FRIOR PILING DATE: 1999-09-18

FRIOR PILING DATE: 1999-10-15

FRIOR PILING DATE: 1999-10-15

FRIOR PILING DATE: 1999-10-12

FRIOR PILING DATE: 1999-10-12

FRIOR PILING DATE: 1999-10-12

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FRIOR PILING DATE: 1999-11-20

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FRIOR PILING DATE: 1999-10-15

FRIOR PILING DATE: 1999-11-20

FRIOR PILING DATE: 1999-11-20

FRIOR PILING DATE: 1999-12-02

FRIOR PILING DATE: 1999-12-03

FRIOR FILING DATE: 1999-12-03

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Pred. No. 1e+02;
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Sequence 245, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
                                                                                               Williams, P. Mickey
Wood, William, I.
Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                Tumas, Daniel
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135 HSFAGLASLO 144
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US-09-905-291A-245
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APPLICANT:
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CURRENT FILING DATE: US/09/907,841

FRICR APPLICATION NUMBER: PC7/US00/04414

FRICR FILING DATE: 2000-02-22

FRICR PELICATION NUMBER: US 60/145,688

FRICR FILING DATE: 1999-07-07

FRICR FILING DATE: 1999-07-26

FRICR FILING DATE: 1999-07-28

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-08

FRICR FILING DATE: 1999-09-13

FRICR FILING DATE: 1999-09-13

FRICR FILING DATE: 1999-09-15

FRICR FILING DATE: 1999-09-15

FRICR FILING DATE: 1999-10-05

FRICR FILING DATE: 1999-10-05

FRICR FILING DATE: 1999-10-05

FRICR FILING DATE: 1999-11-29

FRICR FILING DATE: 1999-11-29
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CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                       Length 713;
                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                            Query Match 75.5%; Score 37; DB 3; Best Local Similarity 60.0%; Pred. No. 1e+02; Matches 6; Conservative 4; Mismatches
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botsoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Gerritsen, Mary E
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135 HSPAGLASLO 144
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h LENGTH: 713
HTYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-245
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US-09-907-841-245
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,824

CURRENT FILIDE DATE: 2001-07-17

CURRENT FILING DATE: 2001-07-17

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-30

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PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 
                                            Sequence 245, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pani, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Gao, Wei-Qiang
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITTLE OF INVENTION: Acids Encoding the Same
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4; Mismatches
                                   PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 713
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CURRENT APPLICATION NUMBER: US/09/903,640
CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 245
LENGTH: 713
                         APPLICATION NUMBER: PCT/US99/28565
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A
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Gerritsen, Mary E
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Paoni, Nicholas F.
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Mather, Jennie P
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Best Local Similarity 60.0.
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Botstein, David
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Eaton, Dan L.
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|35 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-245
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Best Local Similarity
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                        Gaps
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                                                                                         Score 37, DB 3; Length 713; Pred. No. 1e+02; 4; Mismatches 0; Indels
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CURRENT PELLING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-02-22

PRIOR PELLOY DATE: 2000-02-22

PRIOR PELLOY DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28313
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Grimaldi, Christopher J.
Grimaldi, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
                                                                                       Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Paoni, Nicholas F.
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Eaton, Dan L.
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135 HSFAGLASLQ 144
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                       ORGANISM: Homo Sapien
US-09-907-841-245
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TYPE: PRT
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1e+02;
4; Mismatches
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CURRENT APPLICATION NUMBER: US/09/906,742

CURRENT FILING DATE: 2001-07-16

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR PELICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR PLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594
      PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PELING DATE: 2099-12-20
PRIOR FILING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/21547
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Publication No. US20030023054A1
BAPPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
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Eaton, Dan L.
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|135 HSFAGLASLQ 144
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US-09-908-093-245
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Matches 6; Conserv
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US-09-906-742-245
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APPLICANT:
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: 09/665,350
OR FILING DATE: 2000-09-18
OR PELICATION NUMBER: PCT/USOO/04414
OR FILING DATE: 2000-02-22
OR APPLICATION NUMBER: US 60/145,698
OR FILING DATE: 1999-07-07
OR APPLICATION NUMBER: US 60/146,222
OR PILING DATE: 1999-07-26
OR PILING DATE: 1999-07-26
OR APPLICATION NUMBER: PCT/US99/20594
OR PILING DATE: 1999-09-08
OR APPLICATION NUMBER: PCT/US99/20594
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/30911
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
   6; Conservative
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Eaton, Dan L.
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Gao, Wei-Qiang
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Score 37; DB 3; Length 713;
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                            PRIOR FILING DATE: 1990-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1990-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1990-07-28
PRIOR PILING DATE: 1990-07-28
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1990-09-13
PRIOR PILING DATE: 1990-09-13
PRIOR PILING DATE: 1990-09-13
PRIOR PILING DATE: 1990-09-15
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PRIOR PILING DATE: 1990-11-29
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PRIOR PILING DATE: 1990-11-20
PRIOR PILING DATE: 1990-11-20
PRIOR PILING DATE: 1990-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1990-12-06
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie
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Eaton, Dan L.
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Pred. No. 1e+02;
4; Mismatches 0; Indels
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 1090-01-05
NUMBER OF SEQ ID NOS: 423

LENGTH: 113
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CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/65,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/0414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 245, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Botstein, David
APPLICANT: Bettein, David
APPLICANT: Bettein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Best Local Similarity 60.0%;
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Gerritsen, Mary E
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|135 HSFAGLASLQ 144
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; ORGANISM: Homo Sapien
US-09-906-742-245
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APPLICANT:
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Gaps

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APPLICANT: Williams, Dante,
APPLICANT: Williams, Dante,
APPLICANT: Williams, Dante,
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 1046-6-11-22
FRICH PAPLICATION NUMBER: US/09/907.942
CURRENT APPLICATION NUMBER: PET/0500/04414
FRICH FILING DATE: 1209-0-12-2
FRICH APPLICATION NUMBER: US 60/146, 688
FRICH FILING DATE: 1209-0-26
FRICH FILING DATE: 1209-0-26
FRICH FILING DATE: 1209-0-26
FRICH FILING DATE: 1209-0-26
FRICH FILING DATE: 1209-0-3-26
FRICH FILING DATE: 1209-0-3-3
FRICH FILING DATE: 1209-0-3-3
FRICH FILING DATE: 1209-0-3-3
FRICH FILING DATE: 1209-0-3-3
FRICH APPLICATION NUMBER: PCT/US99/21090
FRICH PAPLICATION NUMBER: PCT/US99/21091
FRICH PAPLICATION NUMBER: PCT/US99/21091
FRICH PAPLICATION NUMBER: PCT/US99/21091
FRICH PAPLICATION NUMBER: PCT/US99/31091
FRICH FILING DATE: 1209-12-0
FRICH PAPLICATION NUMBER: PCT/US99/31091
FRICH FILING DATE: 1209-12-0
FRICH PAPLICATION NUMBER: PCT/US99/31091
FRICH FILING DATE: 1209-12-0
FRICH FILING DATE: 1200-01-05
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60.0%; Pred. No. 1e+02;
iive 4; Mismatches
                                                                                                                                           Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
              Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Mather, Jennie P.
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Best Local Similarity 60.0
Matches 6; Conservative
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|135 HSFAGLASLQ 144
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GRGANISM: Homo Sapien
US-09-907-942-245
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                           APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PRICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR PRILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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Pred. No. 1e+02;
4; Mismatches 0; Indels
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| PRIOR PLINING DATE: 1999-10-05 |
| PRIOR FILING DATE: 1999-10-05 |
| PRIOR FILING DATE: 1999-11-29 |
| PRIOR PLICATION NUMBER: PCT/US99/28113 |
| PRIOR PLICATION NUMBER: PCT/US99/28113 |
| PRIOR FILING DATE: 1999-11-30 |
| PRIOR PLINING DATE: 1999-12-02 |
| PRIOR PLINING DATE: 1999-12-06 |
| PRIOR PLINING DATE: 1999-12-06 |
| PRIOR PLINING DATE: 1999-12-20 |
| PRIOR PLINING DATE: 1999-12-30 |
| PRIOR PLINING DATE: 1999-12-30 |
| PRIOR PLINING DATE: 2000-01-05 |
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Sequence 245, Application US/09907942

Publication No. US20030027146A1

GENERAL INFORMATION:
APPLICANT: Genericch, Inc.
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Efercan, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
                                Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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135 HSFAGLASLO 144
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Best Local Similarity
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ORGANISM: Homo Sapien
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APPLICANT: ROY, MATGATE AND
APPLICANT: Timethy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION NUMBER: US 60/145,698
FRIOR FILING DATE: 1999-00-22
FRIOR FILING DATE: 1999-00-26
FRIOR PELING DATE: 1999-00-18
FRIOR FILING DATE: 1999-00-18
FRIOR FILING DATE: 1999-00-18
FRIOR FILING DATE: 1999-00-15
FRIOR FILING DATE: 1999-10-15
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
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                                                                                                                                          Score 37; DB 3; Length 713;
Pred. No. 1e+02;
4; Mismatches 0; Indels
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Publication No. US20030036061A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, P.
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Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Mather, Jennie P.
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APPLICANT: Ashkenzi, Avi
APPLICANT: Bettein, David
APPLICANT: Beton, Dan L.
APPLICANT: Baton, Dan L.
                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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135 HSFAGLASLQ 144
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; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-245
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: 05/065,350
FRIOR APPLICATION NUMBER: 05/065,350
FRIOR APPLICATION NUMBER: 06/0414, 048
FRIOR APPLICATION NUMBER: 06/0414,048
FRIOR APPLICATION NUMBER: 06/0445,698
FRIOR APPLICATION NUMBER: 06/0445,698
FRIOR PAPLICATION NUMBER: 06/0446,222
FRIOR APPLICATION NUMBER: 06/0446,222
FRIOR APPLICATION NUMBER: 06/0446,222
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR FILING DATE: 1999-07-38
FRIOR FILING DATE: 1999-07-38
FRIOR FILING DATE: 1999-07-38
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR FILING DATE: 1999-07-18
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR APPLICATION NUMBER: PCT/US99/2059
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR APPLICATION NUMBER: PCT/US99/30091
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30099
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30099
FRIOR APPLICATION NUMBER: PCT/US99/30099
FRIOR FILING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/30099
FRIOR FILING DATE: 10090-10-05
FRIOR APPLICATION NUMBER: PCT/US99/30099
FRIOR FILING DATE: 10090-10-05
FRIOR APP
                                                    Sequence 245, Application US/09904859
Publication No. US20030036060A1
MEMERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
                                                                                                                                                                           Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Gao, Wei-Qiang
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                           US-09-904-859-245
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APPLICANT:
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APPLICATION NUMBER: PCT/US99/28565

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1990-12-06
PRIOR PLING DATE: 1990-12-06
PRIOR PLING DATE: 1990-12-06
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Publication No. US20030039969A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bettein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-245
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APPLICANT: Stewart, Timothy A.
APPLICANT: Thums, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Milliam, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1e+02;
4; Mismatches 0; Indels
                                     FRIOR APPLICATION NUMBER: F., C., PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 2090-10-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 245
LENGTH: 713
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CURRENT APPLICATION NUMBER: US/09/904,820
CURRENT PILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28
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Publication No. US20030036094A1
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Botstein, David
APPLICANT: Bensoyers, Luc
APPLICANT: Beanoyers, Luc
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Pan, James
Pan, Nicholas F.
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Gerritsen, Mary E
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Best Local Similarity 60.0
Matches 6; Conservative
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Gao, Wei-Qiang
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135 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-204-245
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-30
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PRIOR PILING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,698
PRIOR FILING DATE: 1999-07-26
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Besnoyers, Iuc
APPLICANT: Bacton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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Williams, P. Mickey
Wood, William, I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Gerritsen, Mary E
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Mather, Jennie P.
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Gao, Wei-Qiang
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|135 HSFAGLASLQ 144
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ORGANISM: Homo Sapien
US-09-906-646-245
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT APPLICATION NUMBER: US/09/906,646
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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        CURRENT APPLICATION NUMBER: US/09/904,786
CURRENT FILING DATE: 2010.07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEC ID NOS: 423
LENGTH: 713
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Gramaldi, Christopher Ju.
Grimaldi, Christopher Ju.
Grimey, Austin L.
Hillan, Kenneth, Ju.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Goddard, A.
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Dan L.
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135 HSFAGLASLQ 144
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                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-786-245
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Best Local Similarity
Matches 6; Conserv
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## APPLICANT: Wood, William, I.
### TTTLE OF INVENTION: Acids Enceding the Same
FITTLE PRINCE APPLICATION WIMBER: US/09/901,786

#### PRINCE APPLICATION WIMBER: US/00/0414

### RICK APPLICATION WIMBER: US/00/0414

### RICK APPLICATION WIMBER: US/00/0416

### RICK APPLICATION WIMBER: US/01/059/2034

### RICK APPLICATION WIMBER: US/01/059/2034

### RICK APPLICATION WIMBER: POT/US99/2034

### RICK APPLICATION WIMBER: POT/US99/2036

### RICK APPLICATION WIMBER: POT/US99/2039

#### RICK APPLICATION WIMBER: POT/US99/2039

#### RICK APPLICATION W
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Publication No. US20030044839A1
GENERAL INFORMATION:
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APPLICANT: ARMenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Enc.
APPLICANT: Beton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filorara
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Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 60.0
Matches 6; Conservative
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| HSFAGLASLQ 144
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ORGANISM: Homo Sapien
US-09-903-786-245
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Pred. No. 1e+02;
4; Mismatches 0; Indels
                                    PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PELING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PLENGTH: 713
APPLICATION NUMBER: US 60/146,222
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Publication No. US20030044793A1
GENERAL INFORMATION:
APPLICANT: Genemech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Besterin, David
APPLICANT: Besterin, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Williams, P. Mickey
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Gerritsen, Mary E.
Goddard, A.
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|35 HSFAGLASLQ 144
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; ORGANISM: Homo Sapien
US-09-906-700-245
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Best Local Similarity
Matches 6; Conserv
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US-09-903-786-245
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APPLICANT: "Milliams, Daniel, Panckey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE BAPERENCE: 10466-11.
FILE BAPERENCE: 10466-11.
FILE BAPERENCE: 10466-11.
FRIOR APPLICATION NUMBER: 1050-00-12.
FRIOR FILING DATE: 1090-0-2.
FRIOR FILING DATE: 1090-0-2.
FRIOR FILING DATE: 1090-0-2.
FRIOR FILING DATE: 1099-0-7.
FRIOR FILING DATE: 1099-0-7.
FRIOR PELLORATION NUMBER: PCT/US99/20394
FRIOR FILING DATE: 1099-0-1.
FRIOR PELLORATION NUMBER: PCT/US99/20394
FRIOR FILING DATE: 1099-10-0.
FRIOR PELLORATION NUMBER: PCT/US99/20394
FRIOR FILING DATE: 1099-11-2.
FRIOR FILING DATE: 1099-12-2.
FRIOR FILING DATE: 1099-12-3.
FRIOR APPLICATION NUMBER: PCT/US99/3099
FRIOR PELLORATION NUMBER: PC
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Publication No. US20030045693A1
SENERAL INFORMATION:
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Paoni, Nicholas F.
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                                                                                                 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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, ORGANISM: Homo Sapien
US-09-903-749A-245
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE BY INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same Prize Priz
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Pred. No. 1e+02;
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                                                       Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                           Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margarec Ann
Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                     Gurney, Austin L.
Hillan, Kenneth, J.
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Best Local Similarity 60.0%;
Matches 6; Conservative
Gerritsen, Mary E.
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135 HSFAGLASLQ 144
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RESULT 47 US-09-903-749A-245 ; Sequence 245, Application US/09903749A

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1e+02;
4; Mismatches
     PRIOR FILLING DAIE: 2001-00-12, PRIOR FILLING DATE: 2000-02-22 PRIOR FILLING DATE: 2000-02-22 PRIOR FILING DATE: 1900-07-22 PRIOR PILLING DATE: 1909-07-07 PRIOR FILLING DATE: 1999-07-07 PRIOR PILLING DATE: 1999-07-26 PRIOR FILLING DATE: 1999-07-26 PRIOR FILLING DATE: 1999-07-26 PRIOR FILING DATE: 1999-07-26 PRIOR FILLING DATE: 1999-09-09 PRIOR FILLING DATE: 1999-09-09 PRIOR FILLING DATE: 1999-09-13 PRIOR FILLING DATE: 1999-09-13 PRIOR FILLING DATE: 1999-09-13 PRIOR APPLICATION NUMBER: PCT/US99/21090 PRIOR APPLICATION NUMBER: PCT/US99/21547
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CURRENT APPLICATION NUMBER: US/09/904,956
CURRENT FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 245, Application US/09904956
Publication No. US20030049622A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Mather, Jennie P.
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Eaton, Dan L.
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135 HSFAGLASLQ 144
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US-09-904-119-245
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Wood, William, I.
ATTILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IIILE OF INVENTION: Acids Encoding the Same
                                                          Gaps
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Similarity 60.0%; Pred. No. 1e+02; 6; Conservative 4; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/904,119

CURRENT FILING DATE: 2001-07-11

PRIOR FILING DATE: 2001-07-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1099-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-18

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-15

PRIOR PLING DATE: 1999-10-15

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PRING DATE: 1999-11-29

PRIOR PRING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR PRING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                              Sequence 245, Application US/09904119
Publication No. US20030049621A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Bestoyers, Luc
APPLICANT: Bestoy Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillarin, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerber, Hanspeter
Gerritsen, Mary E.
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135 HSFAGLASLQ 144
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Query Match
Best Local Similarity
Matches 6; Conserva
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APPLICANT:
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Search completed: April 5, 2006, 17:58:14 Job time : 167 secs
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-00
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
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CURRENT APPLICATION NUMBER: US/09/902,736
CURRENT FILING DATE: 2001-07-10
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RICH APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 245, Application US/09902736 Publication No. US20030049676A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenat, Avi
APPLICANT: Botsein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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135 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homc
US-09-904-956-245
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Pred. No. 1e+02;
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PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FLING DATE: 1999-09-08
PRIOR FLING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-13-30
PRIOR FILING DATE: 1999-12-20
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PRIOR PR
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Best Local Similarity 60.0
Matches 6; Conservative
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CORGANISM: Homo Sapien
US-09-902-736-245
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Sequence 245, App Sequence 245, App Sequence 9997, Ap Sequence 121097, A Sequence 131097, A						13	13,	313	11	92	23	92	29	3 6	64 18	329 482(1	11,	11,5	equence 2291	equence 2,	equence 2, equence 2,	equence 2,	equence 2,	equence 2,	equence 10	equence 10	equence 10,	equence 6,	equence 6,	squence 6, squence 6,	quen	guence 6,
US-09-902-736A-245 US-09-906-722A-245 US-09-949-016-9997 US-09-252-991A-21097 US-09-248-796A-15329	US-09-246-756A-1532	. US-09-701-868-10 . US-09-252-991A-21116 . US-08-907-674-1 . US-09-215-087-1	US-09-391-959-1 US-09-914-286-4 US-09-288-796A-21389	US-09-837-812A-4 US-09-489-039A-10735 US-09-857-612A-8 US-09-857-612A-12	US-08-801-344-9 US-09-498-599-9	US-09-489-039A-13942 US-09-543-681A-4671	US-09-701-868-8 US-08-696-944-19 US-09-949-016-9707	US-08-482-142-31 US-08-478-572-31 US-08-484-296-31	US-08-482-142-11 US-08-482-142-29	US-08-482-142-74 US-08-482-142-92	US-08-478-572-11 US-08-478-572-29 US-08-478-572-74	US-08-478-572-92 US-08-484-296-11	US-08-484-296-29 US-08-484-296-74	US-08-484-296-92 PCT-US95-04481-3	US-09-602-787A-644 US-09-252-991A-18591	US-09-270-767-3298 US-09-270-767-4820	US-08-462-831-11	US-08-461-441-11	PCT-US93-08518-11	US-09-248-796A-22910 US-07-945-288-2	US-08-462-831-2	US-08-461-809-2 US-08-461-441-2	US-08-482-142-2 US-08-478-572-2	US-08-460-040-2 US-08-484-296-2	PCT-US93-08518-2	US-07-945-288-10 US-08-462-831-10	US-08-461-809-10	PCT-US93-08518-10	US-07-945-288-6 US-08-462-831-6	US-08-461-809-6	US-08-482-142-6	US-08-478-572-6 US-08-484-296-6	PCT-US93-08518-6
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37 337 35 35) 4. c	*	3333	3 2 2 2	32	332	3 3 3 3 3 3	888	3 3	333	######################################	121	3 3 3	31	3 3	333	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	333	31
28 33 33			8 E 4 4	4 4 4 1 5 6 4	45	7.4.4 4.8	50 50 51 51	52 53 54	55 56	57 58	59 60 61	63 2 5	4 6 4 13	99 67	89 99	70 72	73	75	77	7.9	80	82	83 84	8 8 8 6	87	88 68 8	06 06	1000	99 99 84 44	ម ១ ១	97	8 6 6 6 6 6	100
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version 5.1.7 - 2006 Biocceleration Ltd.	model	:43:24 ; Search time 47 Seconds (without alignments) 17.591 Million cell updates/sec			residues	chosen parameters: 572060			Bummaries	iaa/5_COMB.pep:*	.cgi.2=/,prodated/1/aa/H_COMB.pep:* .cgii2=//prodatad/1/aa/H_COMB.pep:* .cgii2=/prodatad/1/aa/PCTOS_COMB.pep:*	laa/RE_COMB.pep:* .aa/backfiles1.pep:*	s predicted by chance to have a	l to the score of the result being printed, of the total score distribution.	SUMMARIES	Description	Sequence 4,	Sequence 9,	Sequence 1,	Sequence 5,	Sequence 8,	Sequence 1,	Sequence 1,	Sequence 10, Sequence 10,	Sequence 7,	Sequence 11, Sequence 12,	Sequence 245	Sequence 245	Sequence 245	Seguence 245	Sequence 245	US-09-906-618-245 Sequence 245, App 112-03-906-646-245 Sequence 245, App	Sequence 245

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                                                                                                                     Sequence 4, Application US/10145682A
Patent No. 6720311
GENERAL INFORMATION:
FAPLICANT: Tsai, David,
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pig
LOCATION: 300..309
CTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-145-682A-4
                                                                                                                                                                                                                                                                          FILE REFERENCE: 2-04-1892
CURRENT APPLICATION NUMBER: US/10/145,682A
CURRENT APPLICATION NUMBER: US/10/145,682A
CURRENT FILING DATE: 2002-08-23
FRIOR APPLICATION NUMBER: 09/414,136
FRIOR FILING DATE: 1999-10-07
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
SOFTWARE: Microsoft Word 2001.
ALIGNMENTS
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APPLICANT: Teai, David.

APPLICANT: Teai, David.

APPLICANT: Teai, David.

TITLE OF INVENTION: Plateof.

TITLE OF INVENTION: Thereof.

FILE REFERENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/145,682A

CURRENT PILING DATE: 2001-09
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 1999-10-07

PRIOR PILING DATE: 1999-10-07

PRIOR PILING DATE: 1998-10-07

PRIOR APPLICATION NUMBER: 09/149,878

PRIOR PILING DATE: 1998-09-08

PRIOR PILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: 08/993,432 US-10-145-682A-1 ; Sequence 1, Application US/10145682A ; Patent No. 6720311 311 HSFSGVASVE 320 310 HSFSGVASVE 319 1 HSFSGVASVE 10 1 HSFSGVASVE 10 TYPE: PRT ORGANISM: Unknown FEATURE: RESULT 3 US-08-737-045-13 SEQ ID NO 13 LENGTH: 362 셤 ò ö Gaps Sequence 9, Application US/08483926A
Patent No. 5821227
GENERAL INFORMATION:
APPLICANT: Dense W
TITLE OF INVENTION: MODULATORS OF CYTOKINES OF THE TGF BETA
TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME Query Match 100.0%; Score 49; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00094; Matches 10; Conservative 0; Mismatches 0; Indels CITY: Toronto
CONTRY: Canada
COUNTRY: Canada
ZIP: MEBJICH TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,926A
FILING DATE: 07-UN-1995
CLASSIFICATION: 514 NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: BERESKIN & PARR
STREET: 40 king Street West 1 HSFSGVASVE 10 1 HSFSGVASVE 10 RESULT 2 US-08-483-926A-9

ઠે 셤 ATTORNEY AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-155
TELECOMMUNICATION INFORMATION:

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APPLICANT: Mount Sinai Hospital Corporation
TITLE OF INVENTION: COMPOSITIONS COMPRISING MODULATORS OF CYTOKINES OF THE
TITLE OF INVENTION: TGPD SUPERPAMILY AND A METHOD OF TREATMENT WITH SUCH A
TITLE OF INVENTION: COMPOSITION (AS AMENDED)
FILE REFERENCE: 7933.94USWO
CURRENT APPLICATION NUMBER: US/08/737,045A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         Length 361;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Description of Unknown Organism: Pig US-08-737-045-13
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 49; DB 1;
100.0%; Pred. No. 0.051;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08737045A Patent No. 5981483
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
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US-08-483-926A-9
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Gaps
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Patent No. 582127
GENERAL INFORMATION:
APPLICANT: Dennis, James W.
TITLE OF INVENTION: MODULATORS OF CYTOKINES OF THE TGF BETA
TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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             PRIOR FILING DATE: 1999-10-07
PRIOR PILING DATE: 1999-10-07
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR PILING DATE: 1998-09-08
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR PRIOR DATE: 1998-09-08
PR
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,926A
FILING DATE: 07-JUN-1995
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-155
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BERESKIN & PARR STREET: 40 king Street West CITY: Toronto STATE: Ontaxio COUNTRY: Canada ZIP: MSH 312 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INPORNATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                        TYPE: PRT
ORGANISM: Bovine
LOCATION: 300..309
OTHER INFORMATION: Polypeptide fragment from treatment of fetuin from bovine sera as
OTHER INFORMATION: described in the specification.
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Patent No. 6720311
Patent No. 6720311
APPLICANT: TB31, David.
TITLE OF INVENTION: Thereof.
TITLE OF INVENTION: Thereof.
FILE REFERENCE: 2-04-1892
CURRENT APPLICATION NUMBER: US/10/145,682A
CURRENT APPLICATION WUMBER: 09/902,208
PRIOR APPLICATION WUMBER: 09/912,208
PRIOR FILING DAIE: 2001-07-09
PRIOR FILING DAIE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/414,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Preparation of Invention: Polypeptide for the Treatment of Cancer and a Method of Preparation of Invention: Thereof.

TITLE OF INVENTION: Thereof.

FILE REPERENCE: 2-04-1892

CURRENT APPLICATION NUMBER: US/10/145,682A

CURRENT APPLICATION NUMBER: 09/902,208

PRIOR PILING DATE: 1099-10-07

PRIOR PILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-00-018

PRIOR FILING DATE: 1999-00-018

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Microsoft Word 2001.
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90.0%; Pred. No. 0.0039;
tive 1; Mismatches 0; Indels
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; OTHER INFORMATION: Polypeptide fragment from fetuin.
US-10-145-682A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10145682A Patent No. 6720311
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Word 2001.
SEQ ID NO 1
LENGTH: 10
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Matches 9; Conservative
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1 HTFSGVASVE 10
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Matches 9; Conserv
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TYPE: PRT
ORGANISM: Sheep
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                                                                                                                                                                                                                                                                 93.9%; Score 46; DB 2; Length 359, 90.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tracey, Kevin et al.
TITE OF INVENTION: Prevention of Pregnancy Miscarriages
TITE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
STREET: 2600 Century Square, 1501 Fourth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                         0; Indela
                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/476,919
FILING DATE: 18 September 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSter, Jeffery B.
REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: 0602
TELECPHONE: (206) 628-7711
TELEPHONE: (206) 628-7711
                            HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE:
ORGANISM: human
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pentium PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word
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Patent No. 6117837
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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
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Best Local Similarity 90..
Best Local Similarity 70..
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Best Local Similarity 90...
Best Society 90...
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313 HTFSGVASVE 322
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313 HTFSGVASVE 322
       MOLECULE TYPE: protein
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FRAGMENT TYPE: N
ORIGINAL SOURCE:
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                                                                                                                                                                                  ; OKGAN13F:
US-08-932-871B-1
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US-08-780-311A-1
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US-09-476-919-1
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                                                                                                                                                      Sequence 11, Application US/08737045A
Parent No. 5981481
GENERAL INFORMATION:
APPLICANT: Dennis, James W.
APPLICANT: Denetriou, Michael
APPLICANT: Denetriou, Michael
APPLICANT: Denetriou, Michael
APPLICANT: OWNOSITIONS COMPOSITIONS COMPRISING MODULATORS OF CYTOKINES OF THE
TITLE OF INVENTION: COMPOSITION (AS AMENDED)
FILE REPERENCE: 7933.94USWO
CURRENT APPLICATION NUMBER: US/08/737,045A
CURRENT APPLICATION NUMBER: 1997-03-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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Sequence 1, Application US/08932871B

Patent No. 6011005

GENERAL INFORMATION:

APPLICANT: Tracey, Kevin et al.

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSES:

ANGHT TREMAINE LLP

STATE: Washington

CONTRY: USA

ZIP: 98101-1688

COMPUTER: Pentium FV

COMPUTER: Pentium FV

COMPUTER: Word

CURRENT APPLICATION DATA:

ATTORNEY APPLICATION NUMBER: US/08/932,871B

FILING DATE: 18 September 1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: OGFER, JGÉTEY B.

REGISTRATION:

ATTORNEY/AGENT INFORMATION:

TELEFANDE: (206) 628-7711

TELEFAN: (206) 628-7711

TELEFAX: (206) 628-7769

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: APPLICATION

TELEFAX: (206) 628-7769

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: APPLICATION

SEQUENCE ADDRESSES

LENGTH: APPLICATION

TELEFAX: (206) 628-7769

LENGTH: APPLICATION ADDRESSES

REFERENCE CHARACTERISTICS:

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LENGTH: APPLICATION

REGISTRATION ADDRESSES

REGISTRATION ADDRESSES
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90.0%; Pred. No. 0.21;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Unknown Organism:Bovine
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 90.0.
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313 HTFSGVASVE 322
   313 HTFSGVASVE 322
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ORGANISM: Unknown
                                                                                                RESULT 8
US-08-737-045-11
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US-08-932-871B-1
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LENGTH: 359
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GENERAL INFORMATION:
APPLICANT: TBal, David.
TITLE OF INVENTION: Polypeptide for the Treatment of Cancer and a Method of Prepa:
TITLE OF INVENTION: Thereof.
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Patent No. 5981483
GENERAL INFORMATION:
APPLICANT: Dennis, James W.
APPLICANT: Wount Sinai Hospital Corporation
APPLICANT: Wount Sinai Hospital Corporation
TITLE OF INVENTION: COMPOSITION (AS AMENDED)
FILE OF INVENTION: COMPOSITION (AS AMENDED)
FILE REPERENCE: 7933.940590
CURRENT APPLICATION NUMBER: US/08/737,045A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%; Score 46; DB 1; Length 364; 90.0%; Pred. No. 0.21;
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             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,926A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTOMNEY/AGENT INFORMATION:
NAME: KURYDYK, Linda M.
REGISTRATION NUMBER: 34,971
REGISTRATION NUMBER: 3153-155
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
TELEPAS: (416) 364-7311
TELEPAS: (416) 361-1398
INPORMATION FOR SEO ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: AUTOMATICALIDATE
MATORICATION ACCURATE ANDELS
MATORICALIDATE
MATORICALIDA
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Patent No. 6720311
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Best Local Similarity 90.0
Matches 9; Conservative
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; ORIGINAL SOURCE:
ORGANISM: Sheep
US-08-483-926A-10
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318 HTFSGVASVE 327
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-737-045-10
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LENGTH: 364
TYPE: PRT
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| Sequence 10. Application US/08483926A
| Sequence 10. Application US/08483926A
| Patent No. 5821227
| GENERAL INFORMATION:
| APPLICANT: Dennis, James W. |
| TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME |
| TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME |
| CORRESPONDENCE ADDRESS: | ADDRESSE: BERESKIN & PARR |
| STREET: 40 king Street West |
| CITY: Toronto |
| STATE: Ontexio |
| STATE: Ontexio |
| COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                     GENERAL INFORMATION:
APPLICANT: Tracey, Kevin et al.
APPLICANT: Tracey, Kevin et al.
TITLE OF INVENTION: Complexee and Combinations of Fetuin TITLE OF INVENTION: with Therapeutic Agents
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
STREET: 2600 Century Square, 1101 Fourth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%; Score 46; DB 2; Length 359; 90.0%; Pred. No. 0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                ZUP: 98101-1688
COMPUTER: USA
ZIP: 98101-1688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pentium FC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,311A
FILING DATE: January 8, 1997
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: Oster, Jeffrey B.
REGISTRATION NUMBER: 0106
TELEPOMMUNICATION INFORMATION:
TELEPAX: (206) 628-7699
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: Ilinear
TOPOLOSY: Ilinear
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ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
1, Application US/08780311A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1:|||||||
313 HTFSGVASVE 322
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-780-311A-1
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RESULT 16
US-08-737-045-12
i Sequence 12, Application US/08737045A
i Batent No. 5981483
j GENERAL INFORMATION:
i APPLICANT: Dennis, James W.
APPLICANT: Dennis, James W.
APPLICANT: Mount Sinai Hospital Corporation
APPLICANT: Mount Sinai Hospital Corporation
TITLE OF INVENTION: COMPOSITION COMPRISING MODULATORS OF THE
TITLE OF INVENTION: TGFP SUBERFAMILY AND A METHOD OF TREATMENT WITH SUCH A
TITLE OF INVENTION: COMPOSITION (AS AMENDED)
FILE REFERENCE: 1931-94USWO
CURRENT APPLICATION NUMBER: US/08/737,045A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                         Gaps
                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 352;
Pred. No. 9;
1; Mismatches 1; Indel8
           DB 1; Length 352;
9;
                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Unknown Organism:Rat US-08-737-045-12
           Score 38; DB :
Pred. No. 9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 245, Application US/09907794A Patent No. 6635468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney, Austin L.
Hillan, Kenneth, J.
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           77.6%;
80.0%;
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Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genentech, Inc.
Ashkenazi, Avi
Botstein, David
      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                          306 HAPSPVASVE 315
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                                                                                                 1 HSFSGVASVE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Genentecl
APPLICANT: Ashkena:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-907-794A-245
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Sequence 11, Application US/08483926A
Patent No. 582127
GENERAL INFORMATION:
APPLICANT: Dennis, James W.
TITLE OF INVENTION: MODULATORS OF CYTOKINES OF THE TGF BETA
TITLE OF INVENTION: SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.6%; Score 38; DB 2; Length 10; 80.0%; Pred. No. 0.17; tive 1; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/145,682A
CURRENT APPLICATION NUMBER: US/10/145,682A
CURRENT FILING DATE: 2002.08-23
FRIOR APPLICATION NUMBER: 09/902,208
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 1999-10-07
FRIOR APPLICATION NUMBER: 09/149,878
FRIOR APPLICATION NUMBER: 09/149,878
FRIOR APPLICATION NUMBER: 09/93,432
FRIOR APPLICATION NUMBER: 09/93,432
FRIOR APPLICATION NUMBER: 09/93,432
FRIOR APPLICATION NUMBER: 08/993,432
FRIOR APPLICATION NUMBER: 08/993,432
FRIOR APPLICATION NUMBER: 08/993,432
FRIOR APPLICATION NUMBER: 08/993,432
FRIOR APPLICATION: 09/0000
FRIOR APPLICATION: 00/0000
FRIOR APPLICATION: 00/0000
FRIOR APPLICATION: POLYPEPTIGE fragment from fetuin.
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,926A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: KUIGAGY, Linda M.

REGISTRATION NUMBER: 31,971
REFERENCE/DOCKET NUMBER: 31,971
REFERENCE/DOCKET NUMBER: 31,971
REFERENCE/DOCKET NUMBER: 31,971
TELEPATION NUMBER: 31,971
TELEPATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP. MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BERESKIN & PARR STREET: 40 king Street West CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|| |||||
1 HAFSPVASVE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HSFSGVASVE 10
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Best Local Similarity
Matches 8; Conserv
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US-08-483-926A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-483-926A-11
                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-145-682A-7
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Transmembrane Polypeptides and Nucleic
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                                                                                                                APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Roy, Margaret Ann. APPLICANT: Rewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Wood, William, I. TITLE OF INVENTION: Acreted and Transmembrane F TITLE OF INVENTION: Acreted and Transmembrane F TITLE OF INVENTION: Acids Encoding the Same FILE REPERSENCE: 10466-14
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: DCT/US09/905,125A
CURRENT FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-3
PRIOR PLING DATE: 1999-07-3
PRIOR PLING DATE: 1999-07-3
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIO
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Pred. No. 32;
4; Mismatches
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Sequence 245, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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                                                                      Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Homo Sapien
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TITLE REPERBUCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR PAPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-65

PRIOR PILING DATE: 1999-10-65

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 2000-00-05

PRIOR PILING DATE: 2000-00-05
Acids Encoding the Same
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Patent No. 6664376
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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ORGANISM: Homo Sapien
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Best Local Similarity
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US-09-905-125A-245
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR PILING DATE: 1909-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-02
                                                                                                                       RESULT 20
US-09-906-700-245
; Sequence 245, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Botstein, Avi
, APPLICANT: Botstein, David
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Auerin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Eaton, Dan L.
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Tumas, Daniel
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||| HSFAGLASLQ 144
1 HSFSGVASVE 10
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THILE REPRESENCE: 10466-17

CURRENT PELLING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PELLING DATE: 1999-07-26

PRIOR PELLING DATE: 1999-07-26

PRIOR PELLING DATE: 1999-07-28

PRIOR PELLING DATE: 1999-07-38

PRIOR PELLING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR PELLING DATE: 1999-11-00

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR PELLING DATE: 1999-10-10

PRIOR PELLING DATE: 1999-11-00

PRIOR PELLING DATE: 1999-10-00

PRIOR PELLING DATE: 1999-11-00

PRIOR PELLING DATE: 1999-10-00

PRIOR PELLING DATE: 1999
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                   Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Mather, Jennie P.
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Best Local Similarity 60.0
Matches 6; Conservative
                           Desnoyers, Luc
Eaton, Dan L.
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ORGANISM: Homo Sapien
US-09-902-775A-245
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APPLICANT:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-12
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
SEQ ID NO 245
LENGTH: 713
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PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 60.0
Matches 6; Conservative
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135 HSFAGLASLQ 144
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Eaton, Dan L.
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; ORGANISM: Homo Sapien
US-09-903-603A-245
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APPLICANT: Pani, James
APPLICANT: Pani, James
APPLICANT: Pani, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Timothy A.
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANTON: Secreted and Transmembrane Polypeptides and Nucleic
FILE REPRENCE: GNE: 1618P2C12
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
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Pred. No. 32;
4; Mismatches 0; Indels
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US-09-903-603A-245
; Sequence 245, Application US/09903603A
; Patent No. 6/67995
; GENERAL INFORMATION:
; APPLICANT: Genemech, Inc.
; APPLICANT: Botterin, David
. APPLICANT: Botterin, David
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 245
LENGTH: 713
                                                                                                                                                                                                                                               6; Conservative
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Eaton, Dan L.
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|35 HSFAGLASLQ 144
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                                                                                                                  ; ORGANISM: Homo Sapien
US-09-906-700-245
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Best Local Similarity
Matches 6; Conserva
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                              PILE REFERENCE: 1046b-144
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: CPCT/USOO/04414
PRIOR PILING DATE: 2001-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-12-03
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APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-909-064-245
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APPLICANT: Tumas, Daniel
APPLICANT: Timinism. P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-12-02
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Gerriteen, Mary E.
Goddward, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Paoni, Nicholas F.
Roy, Margaret Ann
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Ashkenazi, Avi
Botstein, David
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Best Local Similarity 60.0
Matches 6; Conservative
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Eaton, Dan L.
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135 HSFAGLASLQ 144
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CORGANISM: Homo Sapien
US-09-904-920A-245
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 32;
4; Mismatches
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CURRENT APPLICATION NUMBER: US/09/906,618

CURRENT PILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US/09/906,618

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

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PRIOR PILING DATE: 1999-09-15

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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
                                                                      Ferrara, Napoleone
Filvaroff, Ellen
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Best Local Similarity 60.0%;
Matches 6; Conservative
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; ORGANISM: Homo Sapien
US-09-906-618-245
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION NUMBER: US/09/905,381A CURRENT APPLICATION NUMBER: US/09/905,381A CURRENT FILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: US 60/143,048 PRIOR PILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR FILING DATE: 1999-07-07 PRIOR PILING DATE: 1999-07-26 PRIOR PILING DATE: 1999-07-26 PRIOR FILING DATE: 1999-07-26 PRIOR FILING DATE: 1999-07-28 PRIOR FILING DATE: 1999-07-28 PRIOR FILING DATE: 1999-09-08 PRIOR FILING DATE: 1999-09-09 PRIOR FILING DATE: 1999-09-09 PRIOR FILING DATE: 1999-09-09 PRIOR FILING DATE: 1999-09-09 PRIOR FILING DATE: 1999-09-13 PRIOR FILING DATE: 1999-09-13 PRIOR PILING DATE: 1999-09-13
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Pred. No. 32;
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
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PRIOR PILING DATE: 1999-12-16
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PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 245
LENGTH: 713
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
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Patent No. 6828146
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
Hillan, Kenneth, J.
                                                                                                                      aoni, Nicholas F.
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                                                            lather, Jennie P.
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135 HSFAGLASLQ 144
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ORGANISM: Homo Sapien
US-09-905-381A-245
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Tumes, Daniel,
APPLICANT: Tumes, Daniel,
APPLICANT: William, P. Mickey,
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,462
CURRENT PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-2
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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US-09-904-462-245
'Sequence 245, Application US/09904462
'Patent No. 6878807
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Eaton, Dan L.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 245
LENGTH: 713
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135 HSFAGLASLQ 144
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                                                             TYPE: PRT
CORGANISM: Homo Sapien
US-09-906-646-245
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CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT APPLICATION NUMBER: US/09/906,646
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-2
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PLING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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PELLING DATE: 1999-11-30
PILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US00/00219
FILING DATE: 2000-01-05
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FILING DATE: 1999-12-20
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US-09-906-646-245
US-09-906-646-245
Sequence 245, Application US/09906646
Pacent No. 6852848
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Danial
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
135 HSFAGLASLO 144
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APPLICANT:
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APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-01-0-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
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Grimaldi, Christopher J.
Gurney, Austin L.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.5
Best Local Similarity 60.0
Matches 6; Conservative
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Eaton, Dan L.
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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|135 HSFAGLASLQ 144
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...mas, Daniel
...mas, Daniel
...miliams, P. Mickey
...cricant: William, P. Mickey
...cricant: Wood, William, I. Nickey
...cricant: Control Secreted and Transmembrane Polypeptides and Nucleic
...cricant: Note 10466-14
...cricant: Control Secreted and Transmembrane Polypeptides and Nucleic
...cricant: Note 10466-14
...cricant: Control Secreted and Transmembrane Polypeptides and Nucleic
...cricant: Number: Double 10466-14
...cricant: Control Secreted and Transmembrane Polypeptides and Nucleic
...cricant: Number: Double 10466-14
...cricant: Number: Control Number: Control Minner Print Of Date: PRIOR PRIOR PRINT APPLICATION NUMBER: Control Minner Print Of Date: PRIOR PRINT APPLICATION NUMBER: Control Minner Print Of Date: Co
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                                                   APPLICATION NUMBER: PCT/US99/28313
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Patent No. 6894148
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillay, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Baton, Dan L.
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; ORGANISM: Homo Sapien
US-09-904-462-245
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Best Local Similarity
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US-09-902-736A-245
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Sequence 15222;
Sequence 15222;
Sequence 15222;
Barent No. 6747137;
GENERAL INFORMATION:
APPLICANT: Kebith Weinstock et al
APPLICANT: Kebith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132;
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13;
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15329
TYPE: PRT
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 21097
SEQ ID NO 21097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 334;
                                                                                                                                                                                                   Score 37; DB 2; Length 857;
Pred. No. 39;
                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Matches 7; Conservative
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462 HSYSGVSSLD 471
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262 HSIAGVGSVE 271
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NAME/KEY: UNSURE
LOCATION: (29)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-21097
                                                                             ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9997
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                        SEQ ID NO 9997
LENGTH: 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 6812339

GENERAL INFORMATION:
PAPELICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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FILE REFERENCE: GNE.1618P2C61
CURRENT APPLICATION NUMBER: US/09/906,722A
CURRENT FILING DATE: 2001-07-14
                                                                                                                            PRIOR PELLIANG DATE: 2001-07-18
PRIOR PELLIANG DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-18
PRIOR PLILING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PELLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-06
PRIOR PELLING DATE: 1
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-09-906-722A-245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 30
US-09-949-016-9997
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SEQ ID NO 245
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Gaps

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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 SEQ ID NOS: 33142 SEQ ID NO 21116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08907674

Patent No. 5919685

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Goreler, Karl J.
APPLICANT: Goreler, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPENDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 33; DB 2; Length 266; 75.0%; Pred. No. 70; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,674
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ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/POSCET UNMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21116
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 HSFSGMGS 179
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Best Local Similarity
Matches 6; Conserv
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; CLONE: 1596452
US-08-907-674-1
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US-08-907-674-1
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Sequence 21116, Application US/09252991A

Sequence 21116, Application US/09252991A

Patent No. 6551795

SERENAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                           VESOLI 3.0

Sequence 11, Application US/09701868

Sequence 11, Application US/09701868

Sequence 11, Application US/09701868

Sequence 11, Application US/09701868

GENERAL INCORMATION: Genes Coding For Tomato Beta-Calactosidase Polypeptides

TITLE OF INVENTION: Genes Coding For Tomato Beta-Calactosidase Polypeptides

FILE REFERENCE: 70608/125670

CURRENT APPLICATION NUMBER: US/09/701,868

FRIOR APPLICATION NUMBER: 60/088,805

PRIOR APPLICATION NUMBER: 60/088,805

PRIOR FILING DATE: 1998-06-09

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09701868
Patent No. 6872813
Patent No. 6872813
Patent No. 6872813
APPLICANT: U.S. Department of Agriculture
APPLICANT: U.S. Department of Agriculture
TITLE OF INVENTION: Genes Coding For Tomato Beta-Calactosidase Polypeptides
FILE REFERENCE: 70608/12550
CURRENT APPLICATION NUMBER: US/09/701,868
CURRENT FILING DATE: 2000-12-05
PRIOR PILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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                                 Gaps
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                            Indels
    Pred. No. 35;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CRGANISM: Lycopersicon esculentum US-09-701-868-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-701-868-10
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.4
Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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US-09-701-868-10
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Gaps
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Nail C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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| Patent No. 6664073
| GENERAL INFORMATION:
| APPLICANT: OMURA, Satoshi
| APPLICANT: OMURA, Satoshi
| APPLICANT: OMURA: Satoshi
| TITLE OF INVENTION: AVERMECTIN AGLYCON SYNTHASE GENES
| FILE REFERENCE: 468-30/PH-775-PCT
| CURRENT APPLICATION NUMBER: US/09/914,286
| CURRENT FILING DATE: 2001-08-24
| PRIOR PPLICATION NUMBER: PCT/JP00/01041
| PRIOR PPLICATION NUMBER: JP 99/46961
| PRIOR PPLICATION NUMBER: JP 99/46961
| PRIOR FILING DATE: 1999-02-24
| NUMBER OF SEQ ID NOS: 16
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 4
| LENGTH: 6239
                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: PEAFESG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
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240 HHFEGIALVE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT14
CLONE: 1596452
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US-09-914-286-4
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09215087

Patent No. 5981244

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Shah, Purvi

APPLICANT: Coteley, Neil C.

TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
                                                                                    Score 33; DB 1; Length 331;
Pred. No. 90;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 33; DB 1; Length 331; 60.0%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/215,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION WUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0362 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/09391959; Patent No. 6071704; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                      67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                             | | |:| ||
240 HHFEGIALVE 249
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                                                                                                                                                                 1 HSFSGVASVE 10
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CLONE: 1596452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Pa.
STATE: C.
COUNTRY:
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US-09-391-959-1
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US-09-215-087-1
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Sequence 10735, Application US/09489039A
Batent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELL!
FILE REPERRNCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10735
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US-09-857-612A-12

i Sequence 12, Application US/09857612A

j Patent No. 6940003

j GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours and Company

TILLE OF INVENTION: Plant Lecithin:Cholesterol Acyltransferases

CURRENT FILING DATE: 2001-10-18

PRIOR PILING DATE: 2001-10-18

PRIOR FILING DATE: 1998-12-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Microsoft Office 97
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Sequence 8, Application US/09857612A
Patent No. 694003
GENERAL INFORMATION:
APPLICANT: B. 1. du Pont de Nemours and Company
TITLE OF INVENTION: Plant Lecithin:Cholesterol Acyltransferases
TITLE REPERENCE: BB1262
CURRENT APPLICATION NUMBER: US/09/857,612A
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/110,782
PRIOR PILING DATE: 1998-12-03
NUMBER OF SEC ID NOS: 15
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                               Length 263;
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Pred. No. 1.9e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.3%; Score 32; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.3%;
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Best Local Similarity :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HSFSGV 6
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US-09-857-612A-8
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LENGTH: 434
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LENGTH: 439
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                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 21389
LENGTH: 205
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APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Plant Lecithin:Cholesterol Acyltransferases
FILE REFERENCE: BB1262
CURRENT PELING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/110,782
PRIOR APPLICATION NUMBER: 60/110,782
PRIOR APPLICATION NUMBER: 60/110,782
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 233
                                            Length 6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 205;
Pred. No. 85;
2; Mismatches 1; Indels
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                                                                                  1; Indels
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                                        Score 33; DB 2; I
Pred. No. 2.3e+03;
1; Mismatches 1;
                                                                                                                                                                                                                                                              Sequence 21389, Application US/09248796A Patent No. 6747137
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Patent No. 6940003
                                    Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                            1 HSFSGVASVE 10
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                                                                                                                      1 HSFSGVAS
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; ORGANISM: Zea mays
US-09-857-612A-4
                                                                                                                                                                                                                                       US-09-248-796A-21389
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US-09-489-039A-10735
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US-09-914-286-4
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; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13942
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NAME: Sara, Challes S.
REPERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
TELEPHONE: 608-831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 608-831-2166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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91 HSFVGLAAV 99
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Matches 6; Conserva
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  GENERAL INFORMATION
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CLASSIFICATION:
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US-09-489-039A-13942
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US-08-801-344-9
Sequence 9, Application US/08801344
Patent No. 6087140:
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL TITLE OF INVENTION: FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pyridine nucleotide transhydrogenase, subunit
ORGANISM: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%; Score 32; DB 2; Length 462; 66.7%; Pred. No. 2.1e+02; tive 2; Mismatches 1; Indels
                                                      Score 32; DB 2; Length 439;
Pred. No. 2e+02;
                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 5377-1914
ZIP: 5377-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,344
                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DeWitt Ross & Stevens S.C. STREET: 8000 Excelsior Drive, Suite 401 CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE:
PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SARA, Charles S.
REFERRNCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
TYPE: poptide

WOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 46
US-02-498-599-9
; Sequence 9, Application US/09498599
; Patent No. 6303352
                                                        Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
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206 HSFGGMVALE 215
                                                                                                                                        1 HSFSGVASVE 10
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91 HSFVGLAAV 99
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Matches 6; Conserv
; ORGANISM: Zea mays
US-09-857-612A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: WI
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Sequence 13942, Application US/09489039A

Patent NO. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 463
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ORGANISM: B
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                                                                                                                                                                                                                                                                                    STATE: WI
COUNTRY: U.S.A.
ZIP: 53171-1914
COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF
TITLE OF INVENTION: 1.2-PROPANEDIOL FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defitt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
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APPLICANT: John A. HELLIER
APPLICANT: John A. HELLIER
APPLICANT: Jacqueline DE SILVA
ITILE OF INVENTION: No. 5981831e1 Exo-(1-4)-Beta-D Galactanase
NUMBER OF SEQUENCES: 20
CORRESPENDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,944
FILLING DATE: 23-PEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00372
FILLNG DATE: 23-PEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9403423.8
FILLNG DATE: 23-PEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9403423.8
FILLNG DATE: 23-PEB-1995
SEQUENCE CHARACTERISTICS:
INPORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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Pred. No. 4e+02;
0; Mismatches
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Job time : 49 secs
         Susan A. HELLYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.3%;
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amino acid
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Best Local Similarity 70.0
Matches 7; Conservative
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MOLECULE TYPE: protein

US-08-696-944-19
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                                                                                                                                                                                                                        Sequence 4671, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UCLEIC ACID AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: UNMOBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4671
LENGTH: 468
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Sequence 8, Application US/09701868

Sequence 8, Application US/09701868

Sequence 8, Application US/09701868

Sequence 8, Application US/09701868

GENERAL INFORMATION:
TITLE OF INVENTION: Genes Coding For Tomato Beta-Calactosidase Polypeptides
TITLE REPRENCE: 70608/12568

CURRENT APPLICATION NUMBER: US/09/701,868

CURRENT FILING DATE: 2000-12-05

PRIOR FILING DATE: 1998-06-09

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 835
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65.3%; Score 32; DB 2; Length 463;
Best Local Similarity 66.7%; Pred. No. 2.18+02;
Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 2.1e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Lycopersicon esculentum
US-09-701-868-8
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Best Local Similarity 66.7%;
Matches 6; Conservative
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; ORGANISM: Proteus mirabilis
US-09-543-681A-4671
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92 HSFVGLAAV 100
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Adf 30521
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Ada 60323
                          AAY13385
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ABU67440
ABU67440
ABU67488
ABU67496
AABU67386
AABU62485
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ABU62499
ABU62499
ABU62853
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ABU678888
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ADJ26408
ADE79323
ADE79747
ADF30521
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AAE03524
AAB40380
ADN72605
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ADE73958
ADE99512
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ADG40528
ADF73922
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                                   5, 2006, 17:35:24 ; Search time 189 Seconds (without alignments) 23.248 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Ada26731
Abu64678
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Ada26738
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Ada44766
Adv44766
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    GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                            2443163
                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                2443163 seqs, 439378781 residues
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Maximum Match 100%
Listing first 100 summaries
                         protein search, using sw model
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ABUG3697
ADA26733
ADA26733
ADA44760
ADV44765
ADV44764
ABV4024
ABV30555
AAB30555
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ABB78017
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ADD48974
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003s:*
8: geneseqp2003s:*
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ALIGNMENTS

RESULT 1 ABU63696

ABU63696 standard; peptide; 10 AA.

ABU63696;

11-OCT-2003 (first entry)

Pig fetuin apoptosis-inducing peptide fragment.

Pig; apoptosis; fetuin; cancer; alpha-2-Human serum glycoprotein; alpha-2-HS glycoprotein; foetal protein; tissue remodelling; cell death; embryonic development; supercharged zinc alpha 2-HS glycoprotein; HT-29; colon cancer; LNCaP; prostate cancer; Hep G2; Hepatoma; cytostatic; apoptosis inducer.

Sus scrofa.

US2003087809-A1.

38-MAY-2003

08-OCT-2002; 2002US-00267706.

and inver

97US-00993432. 98US-00149878. 99US-00414136. 2001US-00902208. 14-MAY-2002; 18-DEC-1997; 08-SEP-1998; 07-OCT-1999; 09-JUL-2001;

(TSAI/) TSAI

Tsai D;

WPI; 2003-567578/53.

Process for inducing apoptosis in cancer cells involves use of alpha-2-human serum glycoprotein or its peptide fragment.

Disclosure; Page 11; 27pp; English.

The invention discloses a method for the induction of apoptosis in cancer cells which involves the administration of alpha-2-Human serum (HS) glycoprocein or its peptide fragment to the cancer cells. Alpha-2-HS glycoprotein is a homologue of bovine fetuin, which is a mainly foetal protein and has been shown to control tissue remodelling and physiological cell death during embryonic development, suggesting that it may contain an activity for inducing apoptosis. Methods are also disclosed for the preparation of supercharged zinc alpha 2-HS glycoprotein from alpha 2-HS glycoprotein, which exhibited an increased apoptotic activity. The method is used for inducing apoptosis in cancer cells and treating the cancer. The alpha-2-HS, which has been overloaded with zinc, as well as its fragments, exhibits selectivity for inducing apoptosis in HF-29 (colon cancer), INCaP (prostate cancer) and Hep G2 (Hepatoma) cells, and does not affect CEDIS CO (normal colon) cells. The sequence presented is the pig fetuin apoptosis-inducing peptide fragment

Sequence 10 AA;

Gaps ö ch 100.0%; Score 49; DB 6; Length 10; Similarity 100.0%; Pred. No. 0.0025; 10; Conservative 0; Mismatches 0; Indels Local Similarity Query Match Matches

1 HSFSGVASVE 10

ADA26731 standard; peptide; 10 AA.

ADA26731;

(first entry) 20-NOV-2003

Pig fetuin peptide fragment (FPF).

Pig; colon cancer; prostate cancer; zinc-charged bovine fetuin; fetuin, fetuin,

Sus scrofa.

US2003027767-A1.

06-FEB-2003

14-MAY-2002; 2002US-00145682.

18-DEC-1997; 97US-00993432. 08-SEP-1998; 98US-00149878. 07-OCT-1999; 99US-00414136. 09-JUL-2001; 2001US-00902208.

ö (TSAI/) TSAI Tsai D; WPI; 2003-615747/58.

New compound comprising peptide fragment derived from specially prepared zinc-charged bovine fetuin, useful for treating colon and prostrate cancer, by causing apoptosis in colon cancer and prostate cancer cells.

Example; Page 11; 20pp; English

The invention relates to a compound for treatment of colon and prostate cancer produced from a peptide fragment derived from specially prepared cancer produced from a peptide fragment corresponds to annotate and corresponds to amino acid residues 300-309 of feruin (referred to as fecuin peptide fragment (FPF 300-309)), and human or mouse peptides that correspond to FPF 300-309. The human FPF causes apoptosis in colon cancer cells and prostate cancer cells. The invention also relates to preparing a polypeptide having apoptotic activity isolated from fetuin comprising incubating fetuin in solution with a chelating agent, isolating naked cetuin, incubating the naked fetuin in solution, driving the zinc charged fetuin a solution and classolving the dried zinc charged fetuin in water to form a solution and isolating from the solution, driving the zinc charged fetuin a solution and isolating from the solution the filtrates that have been predetermined to have apoptotic activity in cancer cells. The compound is useful for treating prostate or colon cancer by inducing apoptosis of the cancerous cells. This sequence represents a pig fetuin fragment of the invention.

Sequence 10 AA;

Length 10; 0; Indels 100.0%; Score 49; DB 6; 100.0%; Pred. No. 0.0025; Mismatches ö Conservative Query Match Best Local Similarity Matches 10; Conserv

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Gaps

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RESULT 3

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ADV44763 standard; peptide; 10 AA. ADV44763 ID ADV4 XX

1 HSFSGVASVE 10

US2003087809-A1

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New compound or fetuin polypeptides useful for treating colon and prostate cancer by causing apoptosis in colon and prostate cancer cells, thus offering a breakthrough in cancer therapy.
                                                   fetuin; colon tumor; prostate tumor; neoplasm; apoptosis; cytostatic; protein therapy.
                                 Porcine fetuin fragment FPF 300-09 SEQ ID NO:4.
                                                                                                                                                     18-DEC-1997; 97US-00993432.
08-SEP-1998; 98US-00149878.
07-OCT-1999; 99US-00414136.
09-UUL-2001; 2001US-00902208.
14-MAY-2002; 2002US-00145682.
                                                                                                                                    05-FEB-2004; 2004US-00772537.
                 (first entry)
                                                                                                                                                                                                                                                 WPI; 2005-038780/04.
                                                                                                US2004259800-A1.
                                                                                                                                                                                                           (TSAI/) TSAI D.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 AA;
                10-MAR-2005
                                                                                                                  23-DEC-2004.
                                                                               Sus scrofa.
                                                                                                                                                                                                                               Tsai D;
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The invention relates to a novel compound or fetuin polypeptides for the treatment of colon and prostate cancer, where the polypeptide causes apoptosis in colon and prostate cancer cells. A compound or peptide of the invention has cytostatic activity, and may have a use in protein therapy. The fetuin polypeptides are useful for treating colon and prostate cancer, thus offering a breakthrough in cancer therapy. The present sequence represents the porcine fetuin peptide fragment (FPF) 300-99, amino acids 300-309 of the full-length fetuin polypeptide. 100.0%; Score 49; DB 9; Length 10; 100.0%; Pred. No. 0.0025; tive 0; Mismatches 0; Indels Claim 11; SEQ ID NO 4; 20pp; English.

Best Local Similarity 100 Matches 10; Conservative 1 HSFSGVASVE 10 1 HSFSGVASVE 10 Query Match à 셤

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Gaps

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ABU63698 standard; peptide; 10 AA. 11-OCT-2003 (first entry) ABU63698; RESULT 4 ABU63698

Rat fetuin apoptosis-inducing peptide fragment.

Rat; apoptosis; fetuin; cancer; alpha-2-Human serum glycoprotein; alpha-2-HS glycoprotein; foetal protein; tissue remodelling; cell death; embryonic development; supercharged zinc alpha 2-HS glycoprotein; HT-29; colon cancer; INCaP; prostate cancer; Hep G2; Hepatoma; cytostatic; apoptosis inducer.

Rattus sp

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Cells which involves the administration of alpha-2-Human serum (HS)

'Glycoprotein or its peptide fragment to the cancer cells. Alpha-2-HS

Glycoprotein is a homologue of bovine fetuin, which is a mainly foetal

protein and has been shown to control tissue remodelling and

protein and has been shown to control tissue remodelling and

protein and has been shown to control tissue remodelling and

may contain an activity for inducing apoptosis. Methods are also

disclosed for the preparation of supercharged zinc alpha 2-HS

glycoprotein from alpha 2-HS glycoprotein, which exhibited an increased

apoptotic activity. The method is used for inducing apoptosis in cancer

cells and treating the cancer. The alpha-2-HS, which has been overloaded

with zinc, as well as its fragments, exhibits selectivity for inducing

apoptosis in HT-29 (colon cancer). LNCSP (prostate cancer) and Hep G2

(Hepatoma) cells, and does not affect CED18 CO (normal colon) cells. The

sequence presented is the rat fetuin apoptosis-inducing peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                              The invention discloses a method for the induction of apoptosis in cancer
                                                                                                                                                                                                                                                                               Process for inducing apoptosis in cancer cells involves use of alpha-2-human serum glycoprotein or its peptide fragment.
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                                                                                       18-DEC-1997; 97US-00993432.
08-SEP-1998; 98US-00149978.
07-OCT-1999; 99US-0014136.
09-UUL-2001; 2001US-0092208.
14-MAY-2002; 2002US-00145682.
                                                         08-OCT-2002; 2002US-00267706
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Best Local Similarity
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Sheep; apoptosis; fetuin; cancer; alpha-2-Human serum glycoprotein; alpha-2-HS glycoprotein; foetal protein; tissue remodelling; cell death; embryonic development; supercharged zinc alpha 2-HS glycoprotein; HT-29; colon cancer; LNCaP; prostate cancer; Hep G2; Hepatoma; cytostatic; apoptosis inducer Ovis sp.

08-OCT-2002; 2002US-00267706.

US2003087809-A1.

08-MAY-2003.

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cells which involves the administration of alpha-2-Human serum (HS)

cells which involves the administration of alpha-2-Human serum (HS)

cells which involves the administration of alpha-2-Human serum (HS)

cells which involves the administration of alpha-2-Human serum (HS)

cells an admologue of bovine fecuin, which is a mainly foetal protein and has been shown to control tissue remodelling and and to physiological cell death during embryonic development, suggesting that it of may contain an activity for inducing apoptosis. Methods are also cells contain an activity for inducing apoptosis methods are also control from alpha 2-HS glycoprotein, which exhibited an increased apoptotic activity. The method is used for inducing apoptosis in cancer cells and treating the cancer. The alpha-2-HS, which has been overloaded with zinc, as well as its fragments, exhibits selectivity for inducing apoptosis in HT-29 (colon cancer), INCaP (prostate cancer) and Hep G2 (Hepatoma) cells, and does not affect CEDIS CO (normal.colon) cells. The cangment #1

cells and does not affect CEDIS CO (normal.colon) cells. The cangment #1
                                                                                                                                                                                                                                           invention discloses a method for the induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cow; colon cancer; prostate cancer; zinc-charged bovine fetuin; fetuin; fetuin;
                                                                                                                                                    Process for inducing apoptosis in cancer cells involves use of alpha-2-human serum glycoprotein or its peptide fragment.
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                                                                                                                                                                                                       Disclosure; Page 10; 27pp; English.
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07-OCT-1999; 99US-00414136.
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09-JUL-2001; 2001US-00902208
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                                                    (TSAI/) TSAI D.
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                                                                                     Isai D;
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                                                                                                                                                                                                                                                                                                        The invention discloses a method for the induction of apoptosis in cancer cells which involves the administration of alpha-2-Human serum (HS) of alycoprotein or its peptide fragment to the cancer cells. Alpha-2-HS suproprotein is a homologue of bovine fetuin, which is a mainly foetal protein and has been shown to control tissue remodelling and physiological cell death during embryonic development, suggesting that it may contain an activity for inducing apoptosis. Methods are also disclosed for the preparation of supercharged zinc alpha 2-HS copprotein from alpha 2-HS alycoprotein, which exhibited an increased apoptotic activity. The method is used for inducing apoptosis in cancer cells and treating the cancer. The alpha-2-HS, which has been overloaded with zinc, as well as its fragments, exhibits selectivity for inducing apoptosis in HT-29 (colon cancer). INCaP (prostate cancer) and Hep G2 (Hepatoma) cells, and does not affect CED18 CO (normal colon) cells. The sequence presented is the sheep fetuin apoptosis-inducing peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine; cow; apoptosis; fetuin; cancer; alpha-2-Human serum glycoprotein; alpha-2-HS glycoprotein; foetal protein; tissue remodelling; cell death; embryonic development; supercharged zinc alpha 2-HS glycoprotein; HT-29; colon cancer; LNCaP; prostate cancer; Hep G2; Hepatoma; cytostatic;
                                                                                                                                                                                                                            Process for inducing apoptosis in cancer cells involves use of alpha-2-human serum glycoprotein or its peptide fragment.
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98US-00149878.
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                  18-DEC-1997; 97US-00993432.
08-SEP-1998; 98US-00149878.
07-OCT-1999; 99US-0014136.
09-JUL-2001; 2001US-00992208.
14-WAY-2002; 2002US-00145682.
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New compound comprising peptide fragment derived from specially prepared zinc-charged bovine fetuin, useful for treating colon and prostrate cancer, by causing apoptosis in colon cancer and prostate cancer cells.
                                      Claim 1; Page 13; 20pp; English
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The invention relates to a compound for treatment of colon and prostate cancer produced from a peptide fragment derived from specially prepared and cancer produced from a peptide fragment corresponds to amino acid residues 300-309 of fetuin (referred to as fetuin peptide fragment corresponds to amino acid residues 300-309 of fetuin (referred to as fetuin peptide fragment (FPF 300-309), and human or mouse peptides that correspond to FPF 300-319. The human FPF causes apoptosis in colon cancer cells and prostate cancer cells. The invention also relates to preparing a poptocic activity isolated from fetuin comprising incubating fetuin in solution with a chelating agent, isolating naked fetuin, incubating the maked fetuin in solution with zinc, isolating rainc charged fetuin from the solution, drying the zinc charged fetuin, isolating activity the filtrates that have been predetermined to isolating from the solution the filtrates that have been predetermined to have apoptotic activity in cancer cells. The compound is useful for treating prostate or colon cancer by inducing apoptosis of the cancerous cells. Gaps ô 93.9%; Score 46; DB 6; Length 10; 90.0%; Pred. No. 0.011; ive 1; Mismatches 0; Indels Local Similarity 90.0 Seguence 10 AA; nvention. Query Match

1 HSFSGVASVE 10 |:|||||||| HTFSGVASVE 10 Matches 셤 ઠે

ADA26733 standard; peptide; 10 AA. (first entry) 20-NOV-2003 ADA26733; ADA26733

Rat fetuin peptide fragment (FPF).

Rat; colon cancer; prostate cancer; zinc-charged bovine fetuin; fetuin; fetuin;

Rattus sp.

US2003027767-A1.

14-MAY-2002; 2002US-00145682 06-FEB-2003

18-DEC-1997; 97US-00993432. 08-SEP-1998; 98US-00149878. 07-OZT-1999; 99US-00414136. 09-JUL-2001; 2001US-00902208.

Ġ (TSAI/) TSAI

New compound comprising peptide fragment derived from specially prepared zinc-charged bovine fetuin, useful for treating colon and prostrate cancer, by causing apoptosis in colon cancer and prostate cancer cells.

Example; Page 11; 20pp; English

The invention relates to a compound for treatment of colon and prostate cancer produced from a peptide fragment derived from specially prepared cancer produced from a peptide fragment corresponds to amino acid residues 300-309 of fectuin (referred to as fetuin peptide fragment (PPP 300-309), and human or mouse peptides that correspond to PPF 300-309. The human PPF causes apoptosis in colon cancer cells and

Tsai D;

WPI; 2003-615747/58.

New compound comprising peptide fragment derived from specially prepared zinc-charged bovine fetuin, useful for treating colon and prostrate cancer, by causing apoptosis in colon cancer and prostate cancer cells.

Example; Page 11; 20pp; English

The invention relates to a compound for treatment of colon and prostate cancer produced from a peptide fragment derived from specially prepared zinc-charged bovine fetulin, where the peptide fragment corresponds to amino acid residues 300-309 of fetuin (referred to as fetuin peptide fragment (FPF 300-309), and human or mouse peptides that correspond to fragment (FPF 300-309). The human FPF causes apoptosis in colon cancer cells and prostate cancer cells. The invention also relates to preparing a poptotic activity isolated from fetuin comprising color peptide having apoptotic activity isolated from fetuin comprising color cancer cells and color peptide having apoptotic activity isolated from fetuin comprising fetuin in solution with a chelating agent, isolating naked fetuin in color charged fetuin in water to form a solution and isolating from the solution, driving the zinc charged fetuin in water to form a solution and isolating from the solution the filtrates that have been predetermined to have apoptotic activity in cancer cells. The compound is useful for treating prostate or colon cancer by inducing apoptosis of the invention. ö Sheep, colon cancer, prostate cancer, zinc-charged bovine fetuin, fetuin, fetuin, peptide fragment, FPF, apoptosis. Gaps ö Length 10; 0; Indels 93.9%; Score 46; DB 6; 90.0%; Pred. No. 0.011; 1; Mismatches Sheep fetuin peptide fragment (FPF) ADA26732 standard; peptide; 10 AA. 18-DEC-1997, 97US-00993432. 08-SEP-1998, 98US-00149878. 07-OCT-1999; 99US-00414136. 09-JUL-2001; 2001US-00902208. 14-MAY-2002; 2002US-00145682 20-NOV-2003 (first entry) Query Match
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prostate cancer cells. The invention also relates to preparing a polygeptide having apoptotic activity isolated from fetuin comprising incubating apotectic activity isolated from fetuin comprising fetuin, incubating the naked fetuin in solution with zinc, isolating naked fetuin, incubating the solution, drying the zinc charged fetuin, from the solution, drying the zinc charged fetuin, drying the zinc charged fetuin in water to form a solution and isolating from the solution the filtrates that have been predetermined to thave apoptotic activity in cancer cells. The compound is useful for treating prostate or colon cancer by inducing apoptosis of the cancerous cells. This sequence represents a sheep fetuin fragment of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel compound or fetuin polypeptides for the treatment of colon and prostate cancer, where the polypeptide causes apoptosis in colon and prostate cancer. A compound or peptide of the invention has cytostatic activity, and may have a use in protein therapy. The fetuin polypeptides are useful for treating colon and prostate cancer, thus offering a breakthrough in cancer therapy. The present sequence represents the bovine feuuin peptide fragment (FPF) 300-09, amino acids 300-309 of the full-length fetuin polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1998;
                                                                                                                                                                                                                                                                             10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADV44764;
                                                                                                                                                                                                                                        ADV44765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsai D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
ADV44764
ID ADV44'
XX
AC ADV44'
XX
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09-DEC-2002, 2002WO-GB005571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-APR-2000; 2000WO-US010002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вов вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB30555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                     The invention relates to a novel compound or fetuin polypeptides for the treatment of colon and prostate cancer, where the polypeptide causes apoptosis in colon and prostate cancer cells. A compound or peptide of the invention has cytostatic activity, and may have a use in protein therapy. The fetuin polypeptides are useful for treating colon and prostate cancer, thus offering a breakthrough in cancer therapy. The present sequence represents the ovine fetuin peptide fragment (FPF) 300-09, amino acids 300-309 of the full-length fetuin polypeptide.
                                                                                                                                                                                                                                                               New compound or fetuin polypeptides useful for treating colon and prostate cancer by causing apoptosis in colon and prostate cancer cells, thus offering a breakthrough in cancer therapy.
                                     fetuin; colon tumor; prostate tumor; neoplasm; apoptosis; cytostatic; protein therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mass spectrometry, peptide index; protein identification; protein quantitation; protease; high-resolution mass spectrometry; proteomics; genomics; bioinformatics; Bovine Serum Albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine Serum Albumin indexed peptide database peptide #145.
                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%; Score 46; DB 9; Length 10; 90.0%; Pred. No. 0.011; cive 1; Mismatches 0; Indels
                 Ovine fetuin fragment FPF 300-09 SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                     Example 7; SEQ ID NO 5; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEA78929 standard; peptide; 18 AA.
                                                                                                                                                    08-SEP-1998; 98US-00149978.
07-0CT-1999; 99US-00414136.
09-JUL-2001; 2001US-00902208.
14-MAY-2002; 2002US-00145682.
                                                                                                                         0S-FEB-2004; 2004US-00772537.
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                             WPI; 2005-038780/04.
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HTFSGVASVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSFSGVASVE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 9; Conserv
                                                                                   US2004259800-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003054549-A2.
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 AA;
                                                                                                                                                                                                      (TSAI/) TSAI
                                                                                                     23-DEC-2004.
  10-MAR-2005
                                                                                                                                             18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2005
                                                                 Ovis aries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEA78929;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                          rsai D;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вов
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The invention relates to a novel method of mass spectrometry. The method comprises mass analysing the first molecules in a first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture. The invention further relates to: generating an index constraint in the mass to charge ratios of molecules on index constraints and index to spectrometry by accurately determining the masses or mass to charge carbook first molecules comprising peptide or protein; determining a first physicocomplex in property other than mass or mass to charge ratio of the molecules comprising peptides; and optionally determining a second, third, fourth and/or fifth physico-chemical property of the molecules comprising peptides; and optionally determining a second, third, fourth and/or fifth physico-chemical property of the first molecules or comprising the mass to charge ratio of the first molecules of the basis of the second, third, fourth and/or fifth physico-chemical property and the accurately determined mass to charge ratio of the first molecules and optionally on the basis of the first molecules and optionally on the property. The method and spectrometer are useful in protein cleanification, protein quantitation, proteases, high-resolution mass spectrometry, more mass created by the form an indexed peptide database created by the revenue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                        A method of mass spectrometry, useful in protein identification and quantitation, by mass analyzing the first molecules in the first mixture and accurately determining the mass to charge ratio of the first molecules in the first mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, alpha-2HS-glycoprotein, alpha-2HS; fetuin, alpha-2Z-globulin,
plasma glycoprotein, antiinflammatory; tissue damage; ischemia; stroke,
myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of an alpha-2HS-glycoprotein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel mass spectrometry method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
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Pred. No. 0.021;
                                                                                                                                                                                                         Silva J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.02
1; Mismatches
                                                                                                                                                                                                         Opiteck G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 9B; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB30555 standard; peptide; 341 AA.
08-DEC-2001; 2001US-0340460P.
14-MAR-2002; 2002US-0364847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                 Geromanos S, Dongre A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HSFSGVASVE 10
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                                                                                                                     (MICR-) MICROMASS LTD
                                                                                                                                                                                                                                                                                 WPI; 2003-569290/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200060943-A1.
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This sequence represents a human fetuin polypeptide, a foetal plasma glycoprotein, which is used to help prevent miscarriages during preparery, and for treating pre-term labour during pregnancy. Fetuin acts by suppressing tumour necrosis factor (TNP) secretion by spermine. TNF is secreted by mononuclear cells, and increased levels result in spontaneous
and a therapeutic aromatic or heterocyclic guanyl hydrazone, which is positively charged at physiological pH. The complex has anti-inflammatory activity, based on suppression of pro-inflammatory cytokine synthesis in activated macrophages and other cells (e.g. suppression of TNF-alpha synthesis in LPS-activated macrophages). The presence of fetuin as a drug complex or in combination with the therapeutically active small molecule compound enhances therapeutic activity of the small molecule compound. The present invention further provides a means for screening for therapeutically active small molecule compounds. The present sequence represents human fetuin glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; fetuin; foetal plasma glycoprotein; miscarriage; pregnancy; pre-term labour; tumour necrosis factor; TNF; secretion; spermine; mononuclear cell; spontaneous abortion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of fetuin, a fetal plasma glycoprotein, for prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%; Score 46; DB 2; Length 359; 90.0%; Pred. No. 0.59; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                      Length 359
                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                      Score 46; DB 2;
Pred. No. 0.59;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             AAY07247 standard; peptide; 359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PICO-) PICOWER INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 5; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00932871.
                                                                                                                                                                                                    93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US019579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human fetuin polypeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 90.0 Matches 9; Conservative
                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 HTFSGVASVE 322
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313 HTFSGVASVE 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracey KJ, Wang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 359 AA;
                                                                                                                                                                          Sequence 359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      miscarriages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9913897-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                            AAY07247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                    The present sequence represents a fragment of the bovine alpha-2HS-glycoprotein (alpha-2HS) (HS not defined). The polypeptide is also known as fetuin, alpha-2Z-globulin. The polypeptide is a plasma glycoprotein. Alpha-2HS is a major protein occurring in human blood and calciferous tissues. The polypeptide is an antinflammatory activity potentiator. It is used for treating or inhibiting tissue damage caused by ischemia which is manifest as stroke or as myocardial infarction. Administration of alpha-2HS was found to suppress production of tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complex or combination of guanyl-hydrazone compound - with glycosylated polypeptide, especially fetuin, providing enhanced anti-inflammatory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel complex which comprises a glycosylated peptide selected from mammalian fetuin and/or alpha 2-HS glycoprotein,
                                                                                                                                            Novel methods for treating tissue ischemia or inhibiting tissue damage associated with ischemia, of the brain and heart in a subject involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fetuin; anti-inflammatory; guanyl-hydrazone; glycosylated; cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 4; Length 341; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                            associated with ischemia, of the brain and administering human alpha-2HS-glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                          Disclosure; Page 12-13; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 18; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW61491 standard; protein; 359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human fetuin glycoprotein type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PICO-) PICOWER INST MEDICAL RES
                                                 (PICO-) PICOWER INST MEDICAL RES.
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                      99US-0129288P.
                                                                                                                                                                                                                                                                                                                                                                                                                             93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha 2-HS glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTFSGVASVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HSFSGVASVE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-399059/34.
                                                                                                               WPI; 2001-006853/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1997;
                      13-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9830583-A1
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                                                                                  3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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The invention relates to methods and constructs for protein expression, in particular, the expression of Glial Growth Factor 2 (GGF2). The method comprises transforming a mammalian host cell with an expression vector containing an expressible mammalian fetuin gene and transforming the same mammalian host cell with an expression vector containing an expressible gene which encodes the desired protein, culturing the transformed host cells and isolating the desired protein. The present sequence represents a bovine fetuin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for isolating a desired protein from a mammalian host cell, using an expression vector containing a fetuin gene, useful for production of
                                                                                                                          Glial Growth Factor 2; GGF2; protein expression; fetuin; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.9%; Score 46; DB 3; Length 359; 90.0%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches

    .18
    /note= "signal peptide"

                                                                                                                                                                                                                       19. .359
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 30-32; 40pp; English.
                                                                                                                                                                                  Location/Qualifiers
                        AAYS6990 standard; protein; 359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB78019 standard; protein; 359 AA.
                                                                                                                                                                                                                                                                                                                99WO-US015367
                                                                                                                                                                                                                                                                                                                                          98US-00124605
                                                                                                                                                                                                                                                                                                                                                                                           Chan SY, Tran V, Cheng S;
                                                                          (first entry)
                                                                                                   Bovine fetuin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 HTFSGVASVE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glial Growth Factor 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-195287/17.
                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ56932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 359 AA;
                                                                                                                                                                                                                                                            WO200006713-A2
                                                                                                                                                                                                                                                                                                               08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                         28-JUL-1998;
                                                                        08-MAY-2000
                                                                                                                                                                                                                                                                                       10-FEB-2000.
                                                 AAY56990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                       Protein
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RESULT 17
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            AAY56990
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The present sequence represents a bovine alpha2-Heremans Schmid
Glycoprotein (AHSG). The human Ahsg gene is located on chromosome 3q27.
AHSG inhibits insulin-induced autophosphorylation of the insulin receptor
and insulin receptor tyrosine kinase (H-TK) activity. Genetic ablation
of the Ahsg gene enhances insulin signal transduction and increases whole
co the Ahsg gene enhances insulin signal transduction and increases whole
co transity insulin sensitivity. The phosphorylation status of AHSG is critical
for IR-TK inhibition. The human AHSG protein exists in 2 variant forms.
Cariant AHSG*1 (ABB7014) has a Thr at position 248 and Thr at position
caposition 256. Variant AHSG*2 (ABB78015) has a Met at position 248 and Ser at
phosphorylation of tyrosine kinase activity in a cell augments
phosphorylation or tyrosine kinase activity of insulin receptors in
clave/muscle cell. AHSG modulators can therefore be used for treating
obesity and insulin resistance, increasing insulin sensitivity,
coperum and insulin insuling effect of high-fat diet on body weight gain, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting alpha 2-Heremans Schmid Glycoprotein activity, augmenting phosphorylation/tyrosine kinase activity of insulin receptors, or treating obesity and insulin resistance, by inhibiting AHSG activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; apoptosis; fetuin; cancer; alpha-2-Human serum glycoprotein; alpha-2-HS glycoprotein; foetal protein; rissue remodelling; cell death; embryonic development; supercharged zinc alpha 2-HS glycoprotein; HT-29; colon cancer; LNCaP; prostate cancer; Hep G2; Hepatoma; cytostatic;
Human; alpha2-Heremans Schmid Glycoprotein; AHSG; chromosome 3q27;
insulin; autophosphory/lation; insulin receptor; insulin sensitivity;
insulin receptor tyrosine Kinase; IR-TK; insulin signal transduction;
obesity; insulin resistance; body weight; body fat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                     Goustin AS, Srinivas PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 5; Length 359;
Pred. No. 0.59;
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1; Mismatches
                                                                                                                                                    1. .18
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                   Jen KC,
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 14-15; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   owering total body fat content
                                                                                                                                                                                                                                                                                  29-OCT-2001; 2001WO-US042832.
                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000US-0243442P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                 Mathews ST,
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                             (UYWA-) UNIV WAYNE STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 359 AA;
                                                                                                                                                                                                       WO200239923-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   Grunberger G,
                                                                                                                                                                                                                                              23-MAY-2002
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                                                                                                                                              Peptide
                                                                                            30s BD
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Gaps

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Bovine alpha2-Heremans Schmid Glycoprotein (AHSG).

22-OCT-2002 (first entry)

us-10-772-537-4.rag

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The invention relates to a compound for treatment of colon and prostate cancer produced from a peptide fragment derived from specially prepared zinc-charged bovine fetuin, where the peptide fragment corresponds to amino acid residues 300-309 of fetuin (referred to as fetuin peptide (fragment (FPF 300-309)), and human or mouse peptides that correspond to FPF 300-309. The human FPF causes apoptosis in colon cancer cells and prostate cancer calls. The invention also relates to preparing a correspond to prostate cancer calls. The invention also relates to preparing a colon propertied having apoptotic activity isolated from fetuin comprising cincubating fetuin in solution with a chelating agent, isolating naked celetuin, incubating the naked fetuin in solution with zinc, isolating ainc charged fetuin in solution with zinc, isolating and coloring the zinc charged fetuin in water to form a solution and isolating from the solution, driving the zinc charged fetuin concers that have been predetermined to have apoptotic activity in cancer cells. The compound is useful for treating prostate or colon cancer by inducing apoptosis of the invention.
                                                                                                                                                                                                                                New compound comprising peptide fragment derived from specially prepared zinc-charged bovine fetuin, useful for treating colon and prostrate cancer, by causing apoptosis in colon cancer and prostate cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetuin; colon tumor; prostate tumor; neoplasm; apoptosis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.6%; Score 38; DB 6; Length 10; 80.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine fetuin fragment FPF 300-09 SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADV44766 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                    Claim 2; Page 13; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-1997; 97US-00993432.
08-SEP-1998; 98US-00149878.
07-OCT-1999; 99US-00414136.
09-JUL-2001; 2001US-00902208.
                                            18-DEC-1997; 97US-00993432.
08-SEP-1998; 98US-00149879.
07-OCT-1999; 99US-00414136.
09-JUL-2001; 2001US-00902208.
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              14-MAY-2002; 2002US-00145682
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Best Local Similarity 80.0
Matches 8; Conservative
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1 HAFSPVASVE 10
                                                                                                                                                                                              WPI; 2003-615747/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                               (TSAI/) TSAI D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-2005
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                                                                                                                                                              Tsai D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
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g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses a method for the induction of apoptosis in cancer cells which involves the administration of alpha-2-Human serum (HS) glycoprotein or its peptide fragment to the cancer cells. Alpha-2-HS clycoprotein is a homologue of bovine fetuin, which is a mainly foetal protein and has been shown to control tissue remodelling and planally footal physiological cell death during embryonic development, suggesting that it may contain an activity for inducing apoptosis. Methods are also disclosed for the preparation of supercharged zinc alpha 2-HS glycoprotein from alpha 2-HS glycoprotein, which exhibited an increased supprotic activity. The method is used for inducing apoptosis in cancer cells and treating the cancer. The alpha-2-HS, which has been overloaded with zinc, as well as its fragments, exhibits selectivity for inducing capoptosis in HT-29 (colon cancer), LNCAP (prostate cancer) and Hep G2 (Hepatoma) cells, and does not affect CEDIB CO (normal colon) cells. The sequence presented is the mouse fetuin apoptosis-inducing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse, colon cancer, prostate cancer, zinc-charged bovine fetuin, fetuin, fetuin, fetuin,
                                                                                                                                                                                                                                                                                                                                                                      Process for inducing apoptosis in cancer cells involves use of alpha-2-human serum glycoprotein or its peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.51;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 11; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA26734 standard; peptide; 10 AA.
                                                                                                                                                             18-DEC-1997; 97US-00993412.
08-SEP-1998; 98US-00149978.
07-OCT-1999; 99US-00141136.
09-JUL-2001; 2001US-0092208.
14-MAY-2002; 2002US-00145682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.6%;
80.0%;
                                                                                                                               08-OCT-2002; 2002US-00267706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
apoptosis inducer
                                                             US2003087809-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
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                                                                                                                                                                                                                                                                 (TSAI/) TSAI D.
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                             Mus sp.
                                                                                                                                                                                                                                                                                                    Tsai D;
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Matches
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Gaps

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1; Indels

Pred. No. 0.51; 1; Mismatches

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The human Ahsg gene is located on chromosome 3q27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                           8; Conservative
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                                                                                                                                                                                                                                                                                                                                303 HAFSPVASVE 312
                                                                                                                                                                                                                                                                                                   1 HSFSGVASVE 10
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                    Sequence 346 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grunberger G,
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                                                                                                                                                                                         The invention relates to a novel compound or fetuin polypeptides for the treatment of colon and prostate cancer, where the polypeptide causes apoptosis in colon and prostate cancer cells. A compound or peptide of the invention has cytostatic activity, and may have a use in protein therapy. The fetuin polypeptides are useful for treating colon and prostate cancer, thus offering a breakthrough in cancer therapy. The present sequence represents the murine fetuin peptide fragment (FPF) 300-09, amino acids 300-309 of the full-length fetuin polypeptide.
                                                                                                          New compound or fetuin polypeptides useful for treating colon and prostate cancer by causing apoptosis in colon and prostate cancer cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting alpha 2-Heremans Schmid Glycoprotein activity, augmenting phosphorylation/tyrosine kinase activity of insulin receptors, or treating obesity and insulin resistance, by inhibiting AHSG activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; alpha2-Heremans Schmid Glycoprotein; AHSG; chromosome 3q27;
insulin; autophosphorylation; insulin receptor; insulin sensitivity;
insulin receptor tyrosine kinase; IR-TK; insulin signal transduction;
obesity; insulin resistance; body weight; body fat.
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                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 9; Length 10;
Pred. No. 0.51;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goustin AS,
                                                                                                                          prostate cancer by causing apoptosis in colon a thus offering a breakthrough in cancer therapy.
                                                                                                                                                                   Claim 11; SEQ ID NO 7; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jen KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB78017 standard; protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 14; 70pp; English.
  14-MAY-2002, 2002US-00145682.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                   Similarity 80.08, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         HAFSPVASVE 10
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                                                                                 WPI; 2005-038780/04
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                                                                                                                                                                                                                                                                                                                          Sequence 10 AA;
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                           (TSAI/) TSAI
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Best Local S
                                                       rsai D;
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The present sequence represents a murine alpha2-Heremans Schmid

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AHSG inhibits insulin-induced autophosphorylation of the insulin receptor and insulin receptor tyrosine kinase (IR-TK) activity. Genetic ablation of the Ahsg gene enhances insulin signal transduction and increases whole body insulin sensitivity. The phosphorylation status of AHSG is critical for IR-TK inhibition. The human AHSG protein exists in 2 variant forms. Variant AHSG*1 (ABB7014) has a Thr at position 248 and Thr at position 256. Variant AHSG*2 (ABB7015) has a Met at position 248 and Ser at position 256. Inhibition of AHSG activity in a cell augments phosphorylation or tyrosine kinase activity of insulin receptors in liver/muscle cell. AHSG modulators can therefore be used for treating obesity and insulin resistance, increasing insulin sensitivity, or lowering total body fat content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a rat alpha2-Heremans Schmid Glycoprotein (AHSG). The human Ahsg gene is located on chromosome 3q27. AHSG inhibits insulin-induced autophosphorylation of the insulin receptor and insulin receptor tyrosine kinase (IR-TK) activity. Genetic ablation of the Ahsg gene enhances insulin signal transduction and increases whole body insulin sensitivity. The phosphorylation status of AHSG is critical for IR-TK inhibition. The human AHSG protein exists in 2 variant forms. Variant AHSG*1 (ABB70015) has a Met at position 248 and Thr at position 256. Variant AHSG*2 (ABB78015) has a Met at position 248 and Ser at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting alpha 2-Heremans Schmid Glycoprotein activity, augmenting phosphorylation/tyrosine kinase activity of insulin receptors, or treating obesity and insulin resistance, by inhibiting AHSG activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, alpha2-Heremans Schmid Glycoprotein, AHSG; chromosome 3q27; insulin; autophosphorylation; insulin receptor; insulin sensitivity; insulin receptor tyrosine kinase; IR-TK; insulin signal transduction; obesity; insulin resistance; body weight; body fat.
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                                                                                                                                                                                                                                                                                                                                                                                     Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat alpha2-Heremans Schmid Glycoprotein (AHSG).
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                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition comprising two or more isolated polypeptides, useful for baring a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
position 256. Inhibition of AHSG activity in a cell augments phosphorylation or tyrosine kinase activity of insulin receptors in liver/muscle cell. AHSG modulators can therefore be used for treating obesity and insulin resistance, increasing insulin sensitivity, preventing/diminishing effect of high-fat diet on body weight gain, or lowering total body fat content
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                    Score 38; DB 5; Length 352;
Pred. No. 28;
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                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat Protein A32827, SEQ ID NO 14686.
                                                                                                                                                                                                                                                                                                                                                                       ADD48974 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                    77.6%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                306 HAFSPVASVE 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-268312/26.
                                                                                                                                                                                     Local Similarity
nes 8; Conserv
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                                                                                                                                    Sequence 352 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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29-JAN-2004
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Matches
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activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic construction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of treating an angiogenesis-mediated disorder in a subject. The method is useful for treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovascularisation or diseases associated with chronic inflammation, myocardial ischaemia, stroke, coronary artery disease or peripheral vascular disease. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat; angiogenesis; angiogenesis modulating protein; retinal neovascularisation; choroidal neovascularisation; chronic inflammation; myocardial ischaemia; stroke; coronary artery disease; peripheral vascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF30521 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROC ) PROCTER & GAMBLE CO.
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306 HAFSPVASVE 315
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                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                      Sequence 352 AA;
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Sequence 352 AA;

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Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AlDS; autoinmune disease; rhematoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                              Human secreted protein variant, SEQ ID NO: 210.
                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Komatsoulis GA, Wei P, Baker KP,
                                                                                                                                                                                                                                                                   25-OCT-2000; 2000WO-US029363.
                                                                                                                                                                                                                                                                                          29-OCT-1999; 99US-0162239P. 30-JUN-2000; 2000US-0215139P.
                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
       10-AUG-2001 (first entry)
                                                                                                                                                                                                                 WO200132675-A1.
                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                 gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of treating an angiogenesis-mediated disorder in a subject. The method is useful for treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovasculariation or diseases associated with chronic inflammation, myocardial ischaemia, stroke, coronary artery disease or peripheral vascular disease. The present sequence is used in the exemplification of the invention.
                             Gaps
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   7; Length 352;
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                          Indels
                                                                                                                                                                                                                                angiogenesis; angiogenesis modulating protein;
 Score 38; DB 7
Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greis KD;
                                                                                                                                                                                                          Rat angiogenesis modulating protein #54
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                                                                                                                                ADF30523 standard; protein; 352 AA.
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77.6%;
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26-JUN-2002; 2002US-0391758P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROC ) PROCTER & GAMBLE CO.
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                         8; Conservative
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                                                                      306 HAFSPVASVE 315
                                              1 HSFSGVASVE 10
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N-PSDB; ADF30522.
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rascular disease.
                                                                                                                                                                                                                                                                                                                        US2003162706-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
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The Secreted proteins and their genes are useful fragments or variants.

C AAEDISTA-AAEDIST represent human secreted protein fragments or variants.

CC AAEDISTA-AAEDIST represent human secreted protein fragments or variants.

CC The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 32 genes, continued to the tissues in which they are most highly expressed, and include the new genes. Specific uses are described for each of the 32 genes, calevelophing products for the diagnosis or treatment of proliferative disorders, tumours, focatal and developmental abnormalities.

C develophing products for the diagnosis or treatment of proliferative disorders, diseases of the immune system, AIDS, autoimmune continue disorders, atheristis, inflammation, allergies, cognitive disorders, chizophrenia, asthma, skind disorders, conjuditive disorders, taking disorders, datsorders, datsorders, datsorders, datsorders, datsorders, and datsorders, and disorders, and some also be used to aid wound healing and epithalial cell proteins can also be used to aid wound healing and epithalial cell cognary tissues, to regenerate tissues, to identify their cognate ligands or binding commensation, for supporting cell culture of primary tissues, commensation, and can be used additive or binding commensation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a human secreted protein variant referred to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted
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                                                                                                                                                                 Thirty two human secreted proteins, useful for treating cancers, hyperproliferative disorders, inflammatory disorders, neurological disorders, autoimmune diseases and cardiovascular disorders.
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Young PE;
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 523; 576pp; English
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                                                                                WPI; 2001-328772/34.
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Best Local Similarity
Matches 6; Conserval
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AAE03524 standard; protein; 292 AA.

RESULT 27 AAE03524 AAE03524;

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic, heparotropic, vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; lammunosuppressant; immunostimulant; cardiant; thrombolytic; casqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinfilammatory; antibacterial; cartiviral; antitheumatic; antiinfilammatory; antibacterial; equences can be used for determining the presence of or predisposition to, or preventing or treating parhological conditions associated with an cortain in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, neurodegenerative classed to treat cancers, proliferative disorders, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulnetary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosupunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppresssive; antidialaematory; antiviral; antibacterial; antifungal; antirheumatic; antihfyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotension; neurodegenerative disorder; osteoarthritis; propthyroidism; SciD; AlDS; cardiovascular disease; diabetes mellitus; hypothyroidism; SciD; AlDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; alleryy; aplastic anaemia; nocturnal haemoglobinuia; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF144 polypeptide sequence SEQ ID NO:288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection;
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                                                                                                                                                                                                                                                                                                          AAB40380 standard; protein; 428 AA.
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05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                               134 HSFAGLASLO 143
HSFSGVASVE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up conversediated in transgenic plants overexpressing the heterodimeric ETFAJDB transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal architecture or physiology, altered endoreduplication, biochemistry, signal architecture configuration, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis and special processes such as DNA replication, cell or issues. The identified genes play a cole in a variety of biological processes such as DNA replication as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the EZFA/DPa transcription factor, given in an exemplification of the
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal heemoglobinuria, antiinflammatory disease; to enhance coagulation, to inhibit thrombosis, and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 500.
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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                                                                                                                                            Score 37; DB 3; Length 428;
Pred. No. 57;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                             ADN72605 standard; protein; 460 AA.
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                                                                                                                                              75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                     377 HSYSGVSSLD 386
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                                                                                                                                                                                                                               1 HSFSGVASVE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
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N-PSDB; ADN72604.
                                                                                                                                         Ouery Match
Best Local Similarity
                                                                                                      Sequence 428 AA;
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Yuan J;

Chen J,

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AAY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal to CDNA sequences are obtained from CDNA libraries, prepared from fetal retina. The canoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated crepair of acute and chronic mucosal lesions (e.g. enterocollits, capair of acute and chronic mucosal lesions (e.g. enterocollits, califorentiation (e.g. peoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells and development, diseases, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal carring. PRO265 can be used as a target for anti-tumor drugs. PRO269 can be used as a target for anti-tumor drugs. PRO269 can be used as a target for anti-tumor drugs. PRO313 may chave therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, con be used for related tissue, e.g. in the heart of genital tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic;
                                                                                                                                                                                                                                                                                                               New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 2;
Pred. No. 1e+02;
4; Mismatches 0
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                                                                   970S-0065186P-
970S-0065846P-
970S-006653P-
970S-0066364P-
970S-006646E-
970S-006651P-
970S-0066712P-
970S-0066712P-
970S-0066712P-
970S-0066712P-
                                97US-0064103P.
97US-0064248P.
97US-0064809P.
                     97US-0063870P
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Best Local Similarity 60.0
Matches 6; Conservative
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135 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                 Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO293 protein.
                                                                                                                                                                                                                                                                         WPI; 1999-229533/19.
N-PSDB; AAX52256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 713 AA;
                 31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
                                                                    12-NOV-1997;
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24-NOV-1997
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                                                                                                                                                                                                                                                                                                                   congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
                                                                              Gaps
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                                                                                                                                                                                                                                                                                           Secreted protein; transmembrane protein; human; enterocolitis; Zollinger Ellison syndrome; gastrointestinal ulceration;
                                                    8; Length 460;
                                                                             1; Indels
                                                Score 37; DB 8
Pred. No. 62;
0; Mismatches
                                                                                                                                                                                                                                                                  Amino acid sequence of protein PRO293.
                                                                                                                                                                                      AAY13385 standard; protein; 713 AA.
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97US-0059117P.
97US-0059119P.
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97US-0059122P.
97US-0059184P.
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97US-0059266P.
97US-0062125P.
97US-0062285P.
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97US-0063486P.
97US-0062814P.
97US-0062816P.
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97US-0063120P.
97US-0063121P.
97US-0063127P.
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97US-0063327P.
97US-0063329P.
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97US-0063564P.
97US-0063435P.
97US-0063704P.
                                                 75.5%;
                                                                                                                                                                                                                                                                                                                                                                      wound healing; tissue repair.
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97US-0063735P.
97US-0063738P.
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97US-0063542P.
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                                                            Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                 452 SFSGVVSVE 460
                                                                                                 2 SFSGVASVE 10
                       Sequence 460 AA;
                                                                                                                                                                                                                                        25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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18-SEP-1997;
17-OCT-1997;
17-OCT-1997;
24-OCT-1997;
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24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
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27-OCT-1997;
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 invention.
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Length 713; 0; Indels

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neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic; antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective; thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS; neuropathy; dermal scarring; wound healing; asthma; rhrombosis; bone; cartilage formation; angiogenesis; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; diabetes; stroke; gene therapy; transgenic; PRO; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid encoding a PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                              Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1e+02;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Hillan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; SEQ ID NO 245; 355pp; English.
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                                                                                                                                                                                                                                                                            99WO-US021090.
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135 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-271434/23.
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 713 AA;
                                                                                                                                                                                                       WO200015796-A2.
                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                           16-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                            Chen J,
Yuan J;
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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. esthma. Theumatoid arthritis, multiple sclerosis), inflammatory disparentsum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ME, Goddard A;
Kljavin IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumas D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, Fig 86; 393pp; English.
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                                                                                                                                   2000WO-US004414
                                                                                                                                                                                                  99US-0145698P
99US-0146222P
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99WO-US021090
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99WO-US028214
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99WO-US030095
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N-PSDB; AAF72414.
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Matches 6, Conserv
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                                         WO200104311-A1.
Homo sapiens.
                                                                                                                                   22-FEB-2000;
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                                                                                       18-JAN-2001
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99WO-US021547. 99WO-US028114. 99WO-US028113. 99WO-US028113. 99WO-US028564. 99WO-US028565.

99WO-US030999 2000WO-US000219

99WO-US020594 99WO-US020944

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13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
29-NOV-1999;
30-NOV-1999;
10-DEC-1999;
16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
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                                             Human; PRO; secreted polypeptide; transmembrane polypeptide; pathological disorder; cardiac insufficiency disorder; protein secretion; pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis; skin disease; keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma; cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.
                                                                                                                                                                                                          970S-0059113P.
970S-0059113P.
970S-0059113P.
970S-0059121P.
970S-0059122P.
970S-0059122P.
970S-0059263P.
970S-0062285P.
970S-0062287P.
970S-0062287P.
970S-0062312P.
970S-0062312P.
970S-0063121P.
970S-0063121P.
970S-0063122P.
970S-0063122P.
970S-0063122P.
970S-0063124P.
970S-0063132P.
970S-0063132P.
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97US-0065846P.
97US-0065693P.
97US-0066120P.
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98WO-US019330
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         (first entry)
                             Human PRO polypeptide #42.
                                                                                                                                                 US2002146709-A1.
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                            18 - SER - 1997;

17 - OCT - 1997;

17 - OCT - 1997;

24 - OCT - 1997;

25 - OCT - 1997;

26 - OCT - 1997;

27 - OCT - 1997;

28 - OCT - 1997;

29 - OCT - 1997;

21 - OCT - 1997;

21 - OCT - 1997;

21 - OCT - 1997;

22 - OCT - 1997;

23 - OCT - 1997;

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27 - OCT - 1997;
         16-JUN-2003
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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16-SEP-1998;
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The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polynucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and tumours, in therapeutic treatment of disorders involving pathological cardiacino by the pancreas, including disbetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal celeions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein

Che squamous can be used as molecular markers for protein

Che squamous can be used as molecular markers and call-based assays.

Che sequence represents a human PRO polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrara N;
1 ME, Goddard A;
Kljavin IJ;
Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers L, Eaton DL,
V, Gerber H, Gerritsen |
Gurney AL, Hillan KJ,
F, Roy MA, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi A, Botstein D, Desnoyers L, Filvaroff B, Fong S, Gao W, Gerber H, Godowski PJ, Grimaldi JC, Gurney AL, H Mather JP, Pan J, Paoni NF, Roy MA, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 86; 473pp; English.
                                                                                                                                    02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-UTN-2000; 2000WO-US015584.
28-UTL-2000; 2000WO-US023328.
                                      2000WO-US003565.
2000WO-US004414.
2000WO-US005004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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05-JAN-2000; 2
11-FEB-2000; 2
22-FEB-2000; 2
24-FEB-2000; 2
02-MAR-2000; 2
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; 4; Mismatches 6; Conservative |||:|:||:: 135 HSFAGLASLQ 144 1 HSFSGVASVE 10 Query Match Best Local Similarity Matches 6; Conserv

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Gaps

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Indels

RESULT 34 ABU71486

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The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences are useful in melecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer. Alzheimer's disease or ischaemia, and in various diagnostic assays. ABU71445-ABU71505 represent human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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ID ABU71932 standard; protein; 713 AA.
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 98WO-US025108.
99WO-US020594.
99WO-US0210904.
99WO-US0210904.
99WO-US021813.
99WO-US028113.
99WO-US028113.
99WO-US028165.
99WO-US028565.
99WO-US028565.
99WO-US028565.
99WO-US028565.
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2000WO-US015264.
2000WO-US020710.
2000WO-US023328.
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2000WO-US007377.
2000WO-US008439.
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N-PSDB; ACA58495.
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Best Local Similarity
Matches 6; Conserv
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                                                15.SEP-1999;
15.SEP-1999;
29.NOV-1999;
30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
03-DEC-1999;
04-DEC-1999;
05-DEC-1999;
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                                                                                                                                      Human, secreted and transmembrane protein, PRO polypeptide, cancer, Alzheimer's disease, ischaemia, cytostatic, nootropic, vasotropic,
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ABU71486 standard; protein; 713
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97US-0059115P

97US-0059111P

97US-0059121P

97US-0059122P

97US-0059128P

97US-00622818P

97US-0062281P

97US-0062281P

97US-006281EP

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97US-006281EP

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97US-0063134P

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97US-0066511P.
97US-0066770P.
97US-0066772P.
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98WO-US019177.
98WO-US019330.
98WO-US019437.
                                                                                                                                                                                                                                                                                                          10-JUL-2001; 2001US-00902853
                                                                  10-JUN-2003 (first entry)
                                                                                                    Human PRO polypeptide #42
                                                                                                                                                                        neuroprotective.
                                                                                                                                                                                                                                         US2002192659-A1
                                                                                                                                                                                                         Homo sapiens.
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17.58P.1997
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17.0CT.1997
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21-NOV-1997;
24-NOV-1997;
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24-NOV-1997;
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                                ABU71486;
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Gaps

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Human; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker.
                                 Human secreted/transmembrane protein PRO293.
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9705-0063012P-
9705-0063121P-
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9705-006324P-
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9705-0064103P-
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970S-0059117P.
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97US-0066466P.
97US-0066511P.
97US-0066770P.
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98WO-US018824
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99WO-US020944
                12-JUN-2003 (first entry)
                                                                                                 JS2003003530-A1.
                                                                                Homo sapiens.
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15-OCT-1997,
24-OCT-1997,
24-OCT-1997,
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ABU71932
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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CC of secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO protein extracellular domain. Also included are a vector comprising the PRO polypeptide, and recovering the PRO polypeptide, and recovering the PRO polypeptide (having at least 80% sequence identity to: (a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal competition and sequence, an anti-PRO antibody, detecting a competition and sequence, an anti-PRO antibody, detecting a complaining at least one biological activity of a cell expressing a PRO245 or PRO1868 and modelle to a cell expressing a PRO245 or PRO1868 in a sample suspected of containing the polypeptide or to a PRO biolypeptide or to a cell expressing a PRO245 or PRO1868. Nucleic acids which encode PRO can be used to generate either transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic caids may also be used in gene therapy, in chromosome markers, or in generating probes. The PRO polypeptides are useful may be used for protein electrophoreals, and the isolated
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n ME, Goddard A;
Kljavin IJ;
Tumas D;
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen N
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, 1
Mather JP, Pan J, Booni NF, Roy MA, Stewart TA,
Williams PM, Wood WI;
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                                 99WO-US021547.
99WO-US028014.
99WO-US028114.
99WO-US028301.
99WO-US028564.
99WO-US0380095.
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2000WO-US008437.
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2000WO-US005004
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N-PSDB; ACA60202.
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11-FEB-2000;
24-FEB-2000;
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02-MAR-2000;
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22-MAY-2000;
22-MAY-2000;
28-JUL-2000;
24-AUG-2000;
24-AUG-2000;
15-SEP-1999;
15-SEP-1999;
26-OCY-1999;
30-NOV-1999;
01-DEC-1999;
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16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
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nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents a PRO protein

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                                                                                                                           Human; secreted and transmembrane protein; PRO; pharmaceutical; diagnostic; biosensor; bloreactor; Parkinson's disease; Alzheimer's disease; inflammation; nephritis; wound healing; nerve repair; collateral blood vessel formation; cancer; colorecter; haemorrhage; rheumatoid arthritis; diabetes; cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid; scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
        Gaps
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        Indels
                                                                                                              Novel human secreted and transmembrane protein PRO293.
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 Pred. No. 1e+02;
4; Mismatches
                                                                     ABO01815 standard; protein; 713 AA.
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                                                                                                07-AUG-2003 (first entry)
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Best Local Similarity 60.0
Matches 6; Conservative
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13-SEP-19
15-SEP-19
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(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-370793/35. N-PSDB; ACD07602.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia or strokes.

Claim 12; Fig 86; 482pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-1119 amino acids fully defined in the specification. The PRO polypeptides or polymocleotides are useful as pharmaceuticale, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. Parkinson's disease, Alzheimer's disease, inflammations, nephritis, wound healing, nerve repair, collateral blood vessel formation, cancers (e.g. colorectal cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid arbhritis, diabactes, cirrhosis of the liver, fibrosis of the lungs, restenosis, dermal fibrotic conditions (e.g. keloids or scarring),

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ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats, or rabbits) The PRO polypetides are useful as targets for therapeutic intervention in these diseases, and diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA, or mRNA, The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO; secreted protein; transmembrane protein; enterocolitis; gastrointestinal ulceration; skin disease; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; squamous cell carcinoma; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; inflammatory disease; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; wound repair.
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                                                                                                                                                                                        75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane protein PRO293.
                                                                                                                                                                                                                                                                                                                                                     ABU54388 standard; protein; 713 AA
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97US-0063541P
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                                                                                                                                                                                                     Local Similarity 60.0
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|135 HSFAGLASLQ 144
                                                                                                                                                                                                                                                  1 HSFSGVASVE 10
                                                                                                                                                           Sequence 713 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
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27-OCT-1997;
27-OCT-1997;
28-OCT-1997;
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24-OCT-1997
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New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
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N-PSDB; ABX71650.
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17-0CT-1997
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                                                                                                                                                                                                                                                          24-OCT-1
                                                                                                                                                                                                                                                                                                                                                                                                                      29-0CT-
The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequence given in the specification (appearing as ABU5437-CC ABU54407); (b) an amino acid sequence encoded by the mucleotide sequence consideration (accession numbers in the specification); (c) any one of the PRO sequences which clack its associated signal peptide; (d) an extracellular domain of the PRO polypeptide which lacks its associated signal peptide; (d) an extracellular domain of the PRO polypeptide which lacks its associated stgnal peptide. Also include are the mucleic acids encoding the PRO polypeptides and nucleic acids are useful in diagnosing or treating optopeptides and nucleic acids are useful; and diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as sequences cell carcinoma, Albrehmer's disease, Parkinson's cancers such as sequences cell carcinoma, Albrehmer's disease, e.g. rheumatoid arthritis, athma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature adjng, ADDS, cancer, diabetic complications, or mutations in general. The prolypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The nucleotide sequences may be used antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules are also useful in the development and screening of therapeutically useful reagents, for chromosome addentification, and therapeutically useful reagents, for chromosome addentification of the present sequence assays for PRO, or chromosome addentification of encourate transgenic animals or therapeutically useful reagents, for chromosome addentification of electrophoresis purposes; The anti-PRO antibodies may be used in ceromainer cell culture or natural sources. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, abnormal bleeding; gynaecological disease, asthma, hysterectomy; anglogenesis; coronary ischaemic condition; skin disease; gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; ALS; chronic mucosal lesion; banormal keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease, amyotrophic lateral sclerosis; uncontrolled cell growth, cancer; blood cosquiation cascade; thrombosis; haemorrhage; endometrial bleeding; anglogenesis; wound healing; tumour; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane polypeptide PRO293.
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Claim 12; Fig 86; 473pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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|35 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 713 AA;
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ABO47403
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ABU64540 standard; protein; 713 AA.

RESULT 39 ABU64540 ABU64540;

|||:|:||:| 135 HSPAGLASLQ 144

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The invention relates to an isolated PRO polypeptide. PRO317 is useful in diagnosing or treating abnormal bleeding involved in gynecological diseases e.g. to avoid or lessen the need for hysterectomy. PRO317 may also be useful as an agent that affects angiogenesis and PRO317 is useful in anti-tumour indications or in treating coronary ischaemic conditions. PRO211 and PRO317 polypeptides are useful for treating disorders cassociated with the preservation and maintenance of gastrointestinal macona the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis). PRO3187 polypeptide is useful for treating Parkinson's disease. PRO219 of places, amyotrophic lateral sclerosis (ALS), neuropathies of add disease, amyotrophic lateral sclerosis (ALS), neuropathies compasses, amyotrophic lateral sclerosis (ALS), neuropathies compassed which serves as tumour specific antigens may be cyplypeptide plays a regulatory role in the blood coagulation cascade. PRO346 polypeptide swhich serves as tumour specific antigens may be cyplypeptide is useful as an antithrombotic agent with reduced risk for haemorrhage as compared with hepatin. PRO317 polypeptide is useful in the retain manual prosection have therapeutic applications in wound healing and tissue regular correction have therapeutic applications in wound healing and multiple sclerosis. The polypeptide and untiple sclerosis. The polypeptide and its nucleic acid are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, issues or serum and for a returning corrected, transmembrane PRO polypeptide

Cypresent sequence represents the amino acid sequence of a human secreted/

Cypresent sequence represents the amino acid sequence of a human secreted/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted and transmembrane polypeptides and polymucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 86; 478pp; English.
                                                                                                                                                                               22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US01264.
  99WO-US028313.
99WO-US028301.
99WO-US028564.
99WO-US028565.
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99WO-US030911
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18-SEP-2000; 2000US-00665350.
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Best Local Similarity 60.0%
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1, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                    02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
05-JAN-2000;
11-FEB-2000;
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Filvaroff E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mather JP,
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Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; therapeutic; hyperplasia; endometriosis; cancer; tumour; ischaemia; coronary arterial disease; polycystic kidney disease; renal failure; inflammatory response; asthma; rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy; cytostatic; gynecological; cardiant; nephrotropic; hepatotropic; antiinflammatory.
                                                        Human secreted/transmembrane protein, #44.
                                                                                                                                                                                                                                      9705-0059115P

9705-0059113P

9705-0059113P

9705-0059121P

9705-0059121P

9705-0059124P

9705-0062265P

9705-0062285P

9705-0062285P

9705-0062285P

9705-0063128P

9705-0063121P

9705-0063121P

9705-0063121P

9705-0063124P

9705-0063128P

9705-0063128P

9705-0063128P

9705-006314P

9705-0063128P

9705-0063128P

9705-0063128P

9705-0063128P

9705-0063128P

9705-0063128P

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9705-0063738P
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97US-0066120P.
97US-0066364P.
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                                      13-MAY-2003 (first entry)
                                                                                                                                                                   US2002160374-A1
                                                                                                                                                 Homo sapiens.
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17-SEP-1997;
18-SEP-1997;
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17-0CT-1997;
17-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
29-0CT-1997;
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21-NOV-1997
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Gaps

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The invention discloses isolated PRO secreted/transmembrane polypeptides
and the nucleic acid encoding them. The polypeptides can be used to raise
antibodies that specifically bind to the PRO polypeptide, for linking a
bloactive molecule to a cell expressing a PRO portocin and for linking a
t least one biological activity of a cell. The PRO polypeptides or
c polynucleotides are also useful as pharmaceuticals, diagnostics,
c blosensors or bioreactors, for detecting or treating e.g. hyperplasia,
coronary arterial disease, polycystic kidney disease, chronic or acute
renal failure, or inflammatory responses (e.g. asthma, rheumatoid
arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may
also be used in gene therapy, particularly for replacing a defective
gene. The sequences presented in ABU64499-ABU64559 are the PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245) and genes encoding them, useful for detecting or treating e.g. hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease or inflammations.
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W, Gerber H, Gerritsen
Gurney AL, Hillan KJ,
F, Roy MA, Stewart TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1999; 99W0-US021547.
29-NOV-1999; 99W0-US023089.
29-NOV-1999; 99W0-US028114.
30-NOV-1999; 99W0-US028114.
30-NOV-1999; 99W0-US028114.
30-DEC-1999; 99W0-US028564.
30-DEC-1999; 99W0-US028564.
30-DEC-1999; 99W0-US028565.
30-DEC-1999; 99W0-US0309911.
30-DEC-1999; 99W0-US0309911.
30-DEC-1999; 99W0-US0309911.
30-DEC-1999; 99W0-US0309911.
30-DEC-1999; 99W0-US0309911.
30-DEC-1999; 99W0-US030999.
30-DEC-1999; 99W0-US03099
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97US-0066466P.
97US-006641BP.
97US-006671P.
97US-006772P.
98WO-US018824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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N-PSDB; ABX96219.
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24 - NOV - 1997;
26 - NOV - 1997;
27 - SEP - 1998;
27 - SEP - 1998;
28 - SEP - 1999;
21 - SEP - 1999;
22 - SEP - 1999;
23 - SEP - 1999;
24 - SEP - 1999;
25 - SEP - 1999;
26 - SEP - 1999;
27 - SEP - 1999;
28 - SEP - 1999;
28 - SEP - 1999;
29 - SEP - 1999;
20 - S
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Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D;

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                                                                                                                                                                   Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease; psoriasis; cancer; lung cancer; colon cancer; nerve cell disease; Alzheimer's disease; Parkinson's disease; Usher syndrome; andiogenesis; atrophia areata; inflammatory disease; asthma; rheumatoid arthritis;
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                                                                                       ABU67386 standard; protein; 713 AA
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9705-0062287P

9705-0062287P

9705-0062814P

9705-0062814P

9705-0062814P

9705-0063121P

9705-0063121P

9705-0063121P

9705-0063124P

9705-0063134P

9705-0063134P
                                                                                                                                                 Human secreted protein PRO293
                                                                                                                                                                                                                                                                                         2001US-00906742
                                                                                                                            29-MAY-2003 (first entry)
 6; Conservative
                                     135 HSFAGLASLO 144
                   1 HSFSGVASVE 10
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18-SEP-1997

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24-OCT-1997
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29-OCT-1997;
29-OCT-1997;
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                                                                                                                                                                                                            ischaemia.
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  Matches
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18-NOV-1997;

Score 37; DB 6; Length 713; Pred. No. 1e+02;

75.5%;

Query Match Best Local Similarity

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Gaps

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transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as mucosal lesions e.g. ulears and enterocolitis, skin disease e.g. psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease e.g. Alzheimer's disease and Parkinson's disease usher syndrome, atrophia areata, angiogenesis, inflammatory disease e.g asthma and rheumatoid arthritis, ischaemia, and in various diagnostic assays. The present sequence represents the amino acid sequence of a PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene therapy, tumour, tissue typing, obesity, arthritis, diabetes, hypoinsulinaemia, hyperinsulinaemia, vascular permeability, cardiac insufficiency disorder, immune response, regeneration, cartilage, auditory hair cell, hearing loss, bone disorder; sports injury.
                                                                                                                                                                           75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; ive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                     ABO14906 standard; protein; 713 AA
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970S-0059124P
970S-0059164P
970S-0059263P
970S-006228FP
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Best Local Similarity
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17-SEP-1997;
18-SEP-1997;
18-SEP-1997;
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18-SEP-1997;
17-OCT-1997;
24-OCT-1997;
28-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                   The invention relates to sixty one nucleic acids encoding PRO polyPeptides (secreted and transmembrane). The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Paoni NF, Roy MA, Stewart TA, Tumas D; Wood WI;
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                                                                                                                                                                                                                                                           98US-0113296P.
99US-0143048P.
99US-014622P.
99WO-US02094.
99WO-US02094.
99WO-US02199.
99WO-US02199.
97US-0066120P
97US-006634P
97US-0066468P
97US-006611P
97US-0066772P
97US-006840P
97US-006840P
97US-006840P
97US-006840P
97US-006842P
98US-009803P
98US-0100262P
98US-0100262P
98US-0100262P
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2000WO-US00414.
2000WO-US005004.
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98US-0104080P.
98US-0109304P.
98WO-US025108.
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2000WO-US008439.
2000WO-US014042.
2000WO-US015264.
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99WO-US028564.
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N-PSDB; ACA05540.
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22-FEB-2000;
24-FEB-2000;
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24-AUG-2000;
18-SEP-2000;
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22-MAY-2000;
                        24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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Filvaroff E,
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05-OCT-1999;
29-NOV-1999;
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20-MAR-2000;
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04-JUN-19
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The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide. The polypeptide is useful for identifying agonists of the polypeptide, for preparing variants of the polypeptide, as molecular weight markers for protein electrophoreasis purpose and the nucleic acid is useful for recombinantly expressing those markers. The polypeptide is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The nucleic acid is useful as molecules involved in binding interaction. The nucleic acid is useful as therapeutic actives in the preparation of PRO polypeptide, for antisense RNA and DNA, in the preparation of PRO polypeptide, for antisense RNA and DNA, in the preparation of PRO polypeptide, for antisense the PRO and for the genetic analysis of individuals which is reagents, to construct hybridisation probes for mapping the gene which reagents, to make therapy, for chromosome identification, as chromosome marker, and for generating probes for polymerase chain reaction (PCR), Northern analysis, Southern analysis and Western analysis. PRO antibody is useful for the preparation of medicament for treating to superition of propertide or its antibody e.g. tumour. The polypeptide and the nucleic acid is useful for the preparation of medicament for treating obesity, diabetes or subjective is useful for treating bear typing. The polypeptide is useful for treating bear typing reperted the minner and experience is an uninverse or hypo- or hypo- or hypo- or hypo- or hypo- or described by the en
                               Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; p53 pathway; Leucine rich repeat capricious related protein;
LRRCAPS; cancer; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70. .93
/note= "LRR domain"
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118. .141
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/note= "LRR domain"
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                                                                                                             Claim 12; Fig 86; 469pp; English.
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Best Local Similarity 60.0
Matches 6; Conservative
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N-PSDB; ACD20207
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98WO-US019330.
98WG-US019437.
98WS-0104080P.
98US-0109304P.
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99US-014569BP
99US-0146222P
99WO-US020994
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                                                    970S-0063734P
970S-0063735P
970S-006421SP
970S-006421SP
970S-0064248P
970S-0064248P
970S-0065186P
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20-DEC-1999;
20-DEC-1999;
20-JBC-1999;
11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
20-MAR-2000;
30-MAR-2000;
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29-0CT-1997;
29-0CT-1997;
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31-0CT-1997;
31-0CT-1997;
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07-NOV-1997;
12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
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12-DEC-1997;
04-JUN-1998;
10-SEP-1998;
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24-NOV-1997;
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Human; secreted and transmembrane protein; gene therapy; psoriasis; enterocolitis; gastrointestinal ulceration; skin disease; keratinocyce differentiation; epithelial cancer; Allzheimer's disease; squamous cell carcinome; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility, birth defect; premature aging; AIDS; cancer; diabetic complication; wound repair; tissue re-growth.
                                                                           Novel human secreted and transmembrane protein PRO293.
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9705-0059263P.
9705-0062287P.
9705-0062184P.
9705-0063148P.
9705-0063120P.
9705-0063121P.
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97US-0059122P.
97US-0059184P.
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97US-0059117P.
97US-0059119P.
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970S-0065693P.
970S-0066130P.
970S-0066453P.
970S-0066466P.
970S-0066711P.
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                                                    (first entry)
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18-SEP-1997;
15-OCT-1997;
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24-OCT-1997;
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17-SEP-1997
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28-0CT-15
28-0CT-15
29-0CT-15
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27-OCT-1
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28-OCT-1
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              The invention relates to a method of identifying a candidate p53 pathway modulating agent. The method involves contacting an assay system comprising a purified Leucine rich repeat, capricious related (LRRCAPS) polypeptide or nucleic acid or its fragment with a test agent and detecting a test agent-biased activity, where a difference between the test agent-biased activity, where a difference between the agent based activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent. The method is useful for identifying a candidate p53 pathway-modulating agent for preparing a composition for diagnosing or treating cancer. The invention is useful in gene therapy. The present sequence is human LRRCAPS protein
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Pred. No. 1e+02;
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142. .165
/note= "LRR domain"
166. .189
                                                                     /note= "LRR domain"
214. .237
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                                               'note= "LRR domain"
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15-FEB-2002; 2002US-0357600P.
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Francis-Lang H, Friedman L;
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369. .43
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135 HSFAGLASLQ 144
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Best Local Similarity
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RESULT 43 ABU69663 ID ABU69

Matches

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New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
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n ME, Goddard A;
Kljavin IJ;
Tumas D;
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                                                                                                                                                                                                                                                                                                                  22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
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99WO-US028564.
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99WO-US030095.
99WO-US0309911.
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98WG-01040497.
98US-01040409.
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99WO-US020594.
99WO-US020944.
97US-0066840P.
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98US-0088026P.
98US-0099803P.
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98US-0113296P.
99US-0143048P.
99US-0145698P.
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N-PSDB; ACA55010.
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The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating entercolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzhaimer's disease, Parkinson's disease, amyortrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general The polypeptides are also useful for wound repair and associated therapies concerned with regrowth of tissue. The PRO polypeptides and nucleic acid molecules are

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also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human PRO polypeptide
                                                                                                                           Gaps
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                                                                                                 Score 37; DB 6; Length 713;
Pred. No. 1e+02;
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9705-0059115P.
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9705-0059121P.
9705-0059122P.
9705-0059128P.
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|135 HSFAGLASLQ 144
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Best Local Similarity
Matches 6; Conserv
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17.0CT-1997;
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27-OCT-1997;
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Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.

Claim 12; Fig 86; 467pp; English.

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970S-0063732P
970S-0063734P
970S-0063738P
970S-0064215P
970S-0064215P
970S-0064218P
970S-006428P
970S-006428P
970S-0065846P
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98WS-0100858P
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20-MAR-2000; 2000WO-US007377.
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The invention relates to an isolated secreted and transmembrane PRO polypeptides are useful for modulating biological completed of the properties are useful for modulating biological completed diseases e.g. to avoid or lessen the need for in gynaecological diseases e.g. to avoid or lessen the need for hysterectomy, for treating angiogenesis, tumour, coronary ischaemic condition, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal esions, skin diseases associated with abnormal keratinocyte disease, amyortophic lateral solerosis (ALS), neuropathies, disease colfiferentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's disease, amyortophic lateral solerosis (ALS), neuropathies, disease colfiferential bleeding, wound healing, tissue repair, asthma, rheumatoid carching wound healing, tissue repair, asthma, rheumatoid arthritis, multiple sclerosis Nucleic acid encoding PRO polypeptides are useful in molecular biology including uses as hybridisation probes and in the generation of antisense RNA and DNA, for preparing PRO polypeptides, cor generation of antisense RNA and DNA, for preparing PRO polypeptides, cor generating transgenic animals or knockout animals. The PRO corpieds are useful for immunohistochemical staining and/or assay of antibodies are useful for immunohistochemical staining and/or assay of antibodies are useful for immunohistochemical staining and corpused for affinity purification of PRO form recombinant cell culture or natural constructs. The present sequence represents the amino acid sequence of a human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; secreted; transmembrane; gastrointestinal mucosa, mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticosgulant.
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

Godowski PJ, Grimalál JC, Gul Mather JP, Pan J, Paoni NF, Williams PM, Wood WI;

WPI; 2003-417249/39. N-PSDB; ACD19845.

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9705-0062816P.
9705-0063045P.
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05-JAN-2000; 2000WO-US00229: 11-FEB-2000; 2000WO-US003565. 22-FEB-2000; 2000WO-US0036414. 02-MAR-2000; 2000WO-US005641. 02-MAR-2000; 2000WO-US005841. 03-MAR-2000; 2000WO-US007377. 03-MAR-2000; 2000WO-US012564. 22-MAY-2000; 2000WO-US012564. 28-JUL-2000; 2000WO-US023328. 18-SEP-2000; 2000WO-US023328. 99WO-US030911. 99WO-US030999. 2000WO-US000219. 2000WO-US003565.

(GETH) GENENTECH INC.

Asukenazı A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-765473/72. N-PSDB; ADB29449 Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher syndrome.

Claim 12; Fig 86; 469pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloative molecule to a cell expressing a PRO polypeptides are useful can the aniocule to a cell expressing a PRO polypeptides are useful conformation other PRO polypeptides in a sample and for linking a bloadtive molecule to a cell expressing a PRO polypeptides are useful conformation other PRO polypeptides in a sample and for linking a bloadtive molecule to a cell expressing a PRO polypeptides are useful conformation of a cell expressing PRO polypeptides are also useful conformation of activity of a cell expressing a PRO polypeptides are also useful conformation (c.g. psoriata) bloadied with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal conformation (c.g. psoriata) Parkinson's disease, languages associated with abnormal keratinosotte conformation (c.g. psoriata) parkinson's disease, languages and the relation (c.g. psoriata) parkinson's disease, languages and the relation (c.g. psoriata) parkinson's disease, languages and the relation (c.g. psoriata) in vivo for lessening the effects of viral infection. The PRO polypeptides as tumour specific antiogen which may be exploited as a role in meurodegenerative diseases or their reversal, as an attituromboric agant with reduced risk for haemorrhage as compared with heaperin, in readued risk for haemorrhage as compared and are also encomertial bleeding and openeral and may also have an effect on kidney to cisolate the full-length PRO compared disorders, in modulating of some which have a role in apoptosis. The polymelotedises are useful in molecular bid witch are useful, in the generating reference of the rapeutically useful reagents, as probes and for the genetic animals which are useful an electropheresis are preparable and gene mapping, in the denerating conference of individuals with parel de

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Sequence 713 AA;
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diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PRO polynucleotide of the invention.
                                                                                                                                                                                                       Human, TAT292; cancer; tumour-associated antigenic target; TAT;
breast cancer; ovarian cancer; uterine cancer; tumour; ADEPT; prodrug;
antibody dependent enzyme mediated prodrug therapy.
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                                                                                                                                                                                                                                                                                                         18. .68 ___label= Leucine_rich_repeat_N-terminal_domain
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                                                            Score 37; DB 6;
Pred. No. 1e+02;
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438. .499
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94. .97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label Leucine rich repeat
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| Tabel = Leucine_rich_repeat
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                                                                                                                                                                                                                                                               .. .18
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                                                                                                                                                                                                                                                       location/Qualifiers
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                                                            75.5%;
                                                                                                                                                                           (first entry)
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/label= Le
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label= Le
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'label= Le
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/label= Le
                                                                           6; Conservative
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                                                                                       1 HSFSGVASVE 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                           25-AUG-2003
                                                                                                                                                            ABU62147;
                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                         Domain
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The invention relates to a method of killing a cancer cell, which expresses a tumour-associated antigenic target (TAT) polypeptide, which comprises contacting the cancer cell with an antibody, oligopeptide or organic molecule that binds to the TAT polypeptide on the cancer cell, thus killing the cancer cell. The method is useful for killing cancer cells, particularly breast, ovarian or uterine cancer cells. The method is particularly useful for inhibiting the growth of, treating or preventing tumours or cancers in mammals. This method is also useful for diagnosing the presence of tumours. The anti-TAT antibodise may also be used in Antibody Dependent Ensyme Mediated Produg Therapy (ADEPT) by conjugating the antibody to a prodrug-activating enzyme, which converts a prodrug (e.g. a peptidyl chemocherapeutic agent) to an active anti-cancer associated antigenic target, TAT292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Killing cancer cells (e.g. breast cancer cells), particularly for treating or preventing tumors in mammals, by contacting the cancer cells with an inhibitor (e.g. antibody) of a tumor-associated antigenic target (TAT) polypeptide.
                                                                                     "cAMP and cGMP dependent phosphorylation site"
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                                                                                                                                                                             Tyrosine_kinase_phosphorylation_site
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                                                                                                                                                                                                  555. .558
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/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                             128. .648
| Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-PEB-2000; 2000WO-US004414.
18-SEP-2000; 2000US-0066550.
28-PEB-2001; 2001WO-US0065520.
13-JUL-2001; 2001US-00916583.
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67
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label=
                                                                                  'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-492150/46.
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                                                            Modified-site
                                                                                                        Modified-site
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multiple sclerosis.
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11-FEB-2000; 2
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Filvaroff E,
Godowski PJ,
Mather JP, Pa
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10.SEP-1998;
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13.OCT-1998;
01.DEC-1998;
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08-SEP-1999;
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26-JUL-19
    ö
                                                                                                                                                                                                                                                         Human; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; matkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorthage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                 Gaps
                 ö
                 Indels
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Pred. No. 1e+02;
                 Mismatches
                                                                                                                                                                                                                                 Human secreted/transmembrane protein, #46
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 60.0%;
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|135 HSFAGLASLQ 144
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17. SEP-1997;
17. SEP-1997;
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31-OCT-1997;
03-NOV-1997;
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24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005681.
20-MAR-2000; 2000WO-US0051377.
30-MAR-2000; 2000WO-US008439.
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18-SEP-2000; 2000US-00665350.
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99WO-US028301
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Eaton DL, Ferrara N; , Gerritsen ME, Goddard A; Hillan KJ, Kljavin IJ; Stewart TA, Tumas D; Botstein D, Desnoyers L, Fong S, Gao W, Gerber H, Grimaldi JC, Gurney AL, H an J, Paoni NF, Roy MA, S Pan J, Pao

WPI; 2003-503392/47.

New secreted and transmembrane polypeptides useful for treating skin, neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and

Claim 12; SEQ ID NO 245; 471pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise

11-JUL-2001; 2001US-00903749

US2003045693-A1.

06-MAR-2003

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antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating a tell enate one biological activity of a cell PRO polypeptides are useful to detecting other PRO polypeptides in a sample and for linking a bloactive molecule to a cell expressing a PRO polypeptides are also useful to propeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of a cell expressing PRO polypeptides are lated to uncontrolled cell growth, e.g. cancer. CC differentiation (e.g. psorissis), parkinson's disease, Altheimer's additionally, disease related to uncontrolled cell growth, e.g. cancer. CC differentiation (e.g. psorissis), parkinson's disease, amyotrophic lateral selected with abnormal keratinocyce diseases, amyotrophic lateral selected in monontrolled cell growth, e.g. cancer. CC properties as therapeutic targets for anti-tumour drugs, and are also additionally, disease related to uncontrolled cell growth, e.g. cancer. CC properties as therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine the transputically in vivo for lessening the effects of viral infection. The PRO polypeptides and their portions affect the expression of entithromobetic agent with reduced risk for heamorthage as compared with heparin, in treating other PRO-associated disorders, in modulating of control of properties are note in apoptosis. The polymcloctides are useful in molecular biology including uses as hybridisation probes for control of properties and their portions and for the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals which are useful in the generation of antisense RNA and properties the PRO polypeptides, for generating cransgenic animals and/or assay for PRO ex
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970S-0059115P-970S-0059117P-970S-0059121P-970S-0059124P-970S-0059184P-970S-0059184P-970S-0062818P-970S-0062818P-970S-0062814P-970S-0062814P-970S-0063814P-970S-0063812P-970S-0063812P-970S-0063812P-970S-0063812P-970S-0063812P-970S-006384P-

1997

1997

997

17-0CT-1997; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997;

18-SEP-1997; 18-SEP-1997; 15-OCT-1997; 17-OCT-1997;

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Gaps
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75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; ive 4; Mismatches 0; Indels
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98WO-US018824 98US-0100262P 98WO-US019330 98US-0100858P

10-SEP-1998

24-NOV-1997 24-NOV-1997 25-NOV-1997 04-JUN-1998

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1-NOV-1 8-NOV-1

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98WO-US019177

.6-SEP-1998

98US-0109304P 98WO-US025108 99WO-US020594

98WO-US019437 38US-0104080P

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Human secreted/transmembrane protein PRO293.
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                                17-SEP-2003 (first entry)
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RESULT
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Human; PRO; secreted and transmembrane protein; inflammation; rheumatoid arthritis; psoriasis; multiple sclerosis; atherosclerosis; infertility; birth defect; premature aging; malignancy; cancer; stroke; heart attack; hypertension; gastrointestinal ulceration; Parkinson's disease; Alzheimer's disease; AlDS; cholesterol uptake; wound healing; tissue repair; gene therapy.

Homo sapiens

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Wood WI;
                                                                                   (GETH ) GENENTECH INC.
                                                                                                              WPI; 2003-512316/48.
                                                                                                    Pan J,
                                                                                                                  N-PSDB; ACD66992.
                          02-DEC-1999;
16-DEC-1999;
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                                                                                         Ashkenazi A,
Filvaroff E,
                                                                                                       Williams PM,
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                                                                                                    Mather JP,
                                                                                                                                  mammals
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Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerritsen Caimaldi JC, Gurney AL, Hillan KJ, an J, Paoni NF, Roy MA, Stewart TA, 22-FEB-2000; 2000WO-US004414. 24-FEB-2000; 2000WO-US005004. 02-MAR-2000; 2000WO-US005841. 20-MAR-2000; 2000WO-US007377. 30-MAR-2000; 2000WO-US008439. 22-MAY-2000; 2000WO-US014042. 02-JUN-2000; 2000WO-US01264. 28-JUL-2000; 2000WO-US01264. 99WO-US028214. 99WO-US028313. 99WO-US028364. 99WO-US028565. 99WO-US0208565. 99WO-US021090 99WO-US021547 99WO-US023089 99WO-US030999 2000WO-US000219 2000WO-US003565 24-AUG-2000; 2000WO-US023328. 18-SEP-2000; 2000US-00665350.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO1868), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in

ME, Goddard A; Kljavin IJ; Tumas D; Ferrara N;

Claim 12; Fig 86; 476pp; English.

The invention relates to an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 61 PRO (secreted and transmembrane protein) polypeptides appearing as AB032756-AB032816; or (b) any of 61 nucleotide sequences having 50-4053bp (c) these 61 nucleotide sequences. Also included are the isolated PRO oplypeptide (lacting its associated signal peptide or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide or an extracellular comprising the vector comprising the nucleotide sequence, an anti-PRO antibody, detecting PRO345 or PRO1868 or comprising the vector (nact to propertide), a chimaeric comprising the vector anti-PRO antibody, detecting PRO345 or PRO1868 polypeptide and anti-PRO antibody, detecting PRO345 or PRO1868 polypeptide and modulating at least one biological activity of corporations, linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 polypeptide and modulating at least one biological activity of a cell expressing the PRO245 or PRO1868 polypeptide and modulating at least one biological activity of a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or ploractors. These are useful as particularly useful for diagnostics, multiple sclerosis, infertility, birth defects, premature aging, malignancy e.g. inflammations, rheumatoid arthritis, psoriasis, multiple sclerosis, atherosclerosis, infertility, birth defects, premature aging, malignancy or e.g. cancers), strokes, heart attacks, hypertension, gastrointeetinal ulcerations, Parkinson's diseases, Alzheimer's disease, or AIDS in unammals. These are also useful for modulating cholesterol uptake in the useful in drug screening, the PRO pense park. The PRO pense are useful as phytidisation probes, or for screening probes, or for screening linking energy, particularly for replacing a defective gequence represents a PRO polypeptide are alse useful and p

97US-0063870P

29-OCT-1997; 31-OCT-1997;

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                                                                                                                                                                                            Human, PRO; secreted polypeptide; transmembrane polypeptide; abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion; coronary ischaemic condition; gastrointestinal mucosa; skin disease; ALS; keratinocyte differentiation; psoriasis; Parkinson's disease; asthma; Alzheimer's disease; rheumatoid arthritis; multiple sclerosis; cancer; amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth.
                                          Gaps
                                          ..
0
                       Length 713;
                                         0; Indels
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Pred. No. 1e+02;
                                         Mismatches
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                       75.5%;
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97US-0059117P.
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                                                                                                                                                           (first entry)
                                                                                                                                                                             Human PRO polypeptide #42.
                                          Conservative
                                                                           135 HSFAGLÁSLO 144
                                                          1 HSFSGVASVE 10
              Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                            US2003044793-A1.
       Sequence 713 AA;
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17-SEP-1997;
17-SEP-1997;
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970S-0065846P
970S-0065848P
970S-006584P
970S-0066120P
970S-0066453P
970S-0066451P
970S-0066770P
970S-0066770P
970S-0066770P
970S-0066770P
970S-0066770P
970S-006940EP
970S-006940EP
970S-006940EP
970S-006940EP
970S-0099803P
980S-0099803P
980S-0099803P
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02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US014042.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
                                                                                                                                                                                                 99US-0145698P
99US-0146222P
99WO-US020944.
99WO-US021090.
99WO-US021547.
97US-0064103P.
97US-0064248P.
97US-0064809P.
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99WO-US028564.
99WO-US028565.
99WO-US030095.
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98WO-US019437
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20-DEC-1999;
20-DEC-1999;
05-JAN-2000; 2
11-FEB-2000; 2
22-FEB-2000; 2
                                                      24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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21-NOV-1997;
21-NOV-1997;
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                    12-NOV-1997;
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20-NOV-1998
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Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI;

WPI; 2003-492256/46. N-PSDB; ACD83153.

Novel secreted and transmembrane PRO polypeptides and polynucleotides encoding them, useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.

Claim 12, Fig 86; 475pp; English

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transmenbrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides can be used in diagnosing or treating abnormal bleeding involved in gynacological diseases e.g. to avoid or lessen the need for hysterectomy. They can also be used in preservation and maintenance of gastroincestinal mucosa and the repair of keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, asthma 'rheumatoid arthritis, multiple sclerosis, almostrophic lateral sclerosis (ALS), neuropathies and diseases related to uncontrolled cell growth, such as cancer. Sequences ABO34816-ABO34876 represent human PRO polypeptides of the invention
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                                                                                                                                                                                                                                                                        Gaps
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 The invention relates to human PRO polypeptides (secreted and
                                                                                                                                                                                                                                      75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    0; Indels
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970S-0059117P.
970S-0059119P.
970S-0059121P.
970S-0059124P.
970S-0059124P.
970S-0059124P.
970S-0059124P.
970S-0052184P.
970S-00621814P.
970S-0063144P.
970S-0063114P.
970S-0063114P.
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                                                                                                                                                                                                                                                                     6; Conservative
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|35 HSFAGLASLQ 144
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                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                         Sequence 713 AA;
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L7-SEP-1997
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97US - 0065693P - 97US - 0066120P - 97US - 0066454P - 97US - 0066466P - 97US - 0066411P - 97US - 0066410P - 97US - 0066410P - 97US - 0066440P - 97US - 00664425P - 98US - 0088026P - 2008026P - 2
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97US-0065186P.
97US-0065846P.
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99US-0145698P.
99US-0146222P.
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98WO-US019437
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20-DEC-1999;
05-JAN-2000;
11-FEB-2000;
              27-0CT-1997
28-0CT-1997
28-0CT-1997
28-0CT-1997
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24-NOV-1997;
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12-DEC-1997;
04-JUN-1998;
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15-SEP-1999;
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05-OCT-1999;
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18-SEP-2000;
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12-NOV-1997;
17-NOV-1997;
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21-NOV-1997;
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24-NOV-1997;
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17-SEP-1998;
17-SEP-1998;
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20-NOV-1998;
01-DEC-1998;
22-DEC-1998;
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Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D; Pan J, Pac, Wood WI; (GETH) GENENTECH INC Ashkenazi A, Filvaroff E, Godowski PJ, Williams PM, Mather JP,

WPI; 2003-521801/49. N-PSDB; ADA16280. New genes encoding for secreted and transmembrane PRO polypeptides, useful for treating e.g. cardiac insufficiency disorders, wounds, cancers, obesity, diabetes, hyperinsulinemia, hypoinsulinemia, or arthritis.

Claim 12; SEQ ID NO 245; 476pp; English.

the invention disciplate isolated to the polypoptides can be used to raise and the muclaic acid encoding them. The polypoptides can be used to raise and the muclaic acid encoding them. The polypoptides can be useful as phenomena to the polypoptides are useful as parell for moulating for linking a bloactive molecule to a cell expressing a PRO polypoptides. The PRO polypoptides are useful as pharmaceuticals, diagnostics, blosensors of a cell expressing a PRO polypoptides or the proliferation of the proliferation and/or cells, modulating proliferation and/or cells, modulating or treating or treating cardiac insufficiency disorders, wounds, cancerous cretinitis pigmentosum, obesity, diabetes, hyperinaulinemia, or bone or cartilage disorders (e.g. sports sinjuries or retinitis pigmentosum), obesity, diabetes, hyperinaulinemia, or bone or cartilage disorders (e.g. sports sinjuries or crimitis pigmentosum), obesity, diabetes, hyperinaulinemia, or bone or cartilage disorders (e.g. sports sinjuries or crimitis pigmentosum), obesity, diabetes, hyperinaulinemia, or bone or cartilage disorders (e.g. sports sinjuries or combinantly propressing the process and their portions affect the crimitis pigmentosum, obelity and polypoptides or the development and gene mapping, in the generating transgenic conformation of the propersing the process, as therapoutic The invention discloses isolated PRO secreted/transmembrane polypeptides nvention.

Sequence 713 AA;

ö Gaps ö 75.5%; Score 37; DB 6; Length 713; 60.0%; Pred. No. 1e+02; ive 4; Mismatches 0; Indels Query Match
Best Local Similarity 60.0
Matches 6; Conservative

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